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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Sat May 13 04:41:02 2000; MasPar time 3.04 Seconds 116.737 Million cell updates/sec

Scoring table: Sequence: Description: Perfect Score: >US-08-991-628-2 (1-15) from US08991628.pep 105 1 FGIFVVDKNTGDINI 15

PAM 150 Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seg length 15

Database: a-geneseq35 1:geneseqp

Statistics: Mean 18.538; Variance 60.235; scale 0.308

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					00:::::::			
		æ						
Result		Query						
NO.	No. Score Match Length DB ID	Match	Length	B	ID	Description Pre	Pred. No.	
1	105	105 100.0	15	۳	15 1 W04842	1 105 100.0 15 1 W04842 Self epitope of desmog 3.51e-04	.51e-04	
Note: P	ost-pro	cessor	removed	4	summaries	Note: Post-processor removed 44 summaries from list due to search parameters char	and to to	2

parameters chosen.

ALIGNMENTS

B	PN	လွ	X	X	×ε	XX	KΨ	×	ЭG	ij	AC	Ð	RESULT
12-SEP-1996.	WO9627387-A1.	Homo sapiens.	influenza; haemagglutinin; reovirus; sigma protein.	human papillomavirus; Epstein-Barr virus; DNA polymerase;	herpes simplex virus; adenovirus; phosphomannomutase;	pemphigus vulgaris; desmoglein; multiple sclerosis;	autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte;	Tolerisation; self-epitope; antigen; autoimmune disease;	Self epitope of desmoglein 3, implicated in autoimmune disease.	18-FEB-1997 (first entry)	W04842;	W04842 standard; peptide; 15 AA.	LT 1

PΨ

07-MAR-1996; U03182.

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PA	(HARD) HARVARD COLLEGE.	
ΡI	Strominger JL, Wucherpfennig KW;	
묽	•	
PŢ	Pemphigus vulgaris auto-antigens and multiple sclerosis non-self	
PT	antigens - useful in disease treatment, and method for	
PT	identification of other self and non-self antigens implicated in	
PT	auto-immune disease	
PS	Claim 1; Page 38; 58pp; English.	
င္ပ	Pharmaceutical preparations for tolerisation to antigens comprise	
င္ပ	either an isolated human non-collagen or non-myslin basic protein	
ဂ္ဂ	(MBP) polypeptide which is capable of tolerising an individual to an	
င္ပ	autoantigen; or an isolated human pathogen polypeptide capable of	
င္ပ	tolerising an individual to that polypeptide. In both cases, the	
ဂ	polypeptide (whether self or non-self) includes an amino acid	
င္ပ	sequence corresponding to a sequence motif for a MHC class II	
င္ပ	protein, such as HLA-DR, which is associated with a human autoimmune	
င္ပ	disease and which binds to the polypeptide to activate autoreactive	
င္ပ	T-cells in individuals with the autoimmune disease. This peptide is	
င္ပ	derived from the human desmoglein 3 protein (amino acids 97-111)	
ဌ	and is implicated as a self epitope in pemphigus vulgaris. Peptides	
S	derived from the human desmoglein protein are described in w04841-47.	
SO	Sequence 15 AA;	
ō		
Be	Best Local Similarity 100.0%; Pred. No. 3.51e-04;	

Search completed: Sat May 13 04:41:09 2000 Job time: 7 secs. Matches 1 FGIFVVDKNTGDINI 15 1 FGIFVVDKNTGDINI 15 15; Conservative 0 Mismatches 0 Indels <u>..</u> Gaps

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RESULT ID PROPERTY OF THE PROP
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                                                                                                  Sequence
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   Sequence 2, Application PC/TUS9603182 GENERAL INFORMATION:
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                                                                                                  Application
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Match
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Gap 15
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1:PCT 2:U6 3:U60 4:U7 5:U80 6:U81 7:U82 8:U83 9:U84A
10:U84B 11:U85 12:U86 13:U87 14:U88 15:U89 16:U90 17:U91
18:U92 19:U93 20:U94 21:U95 22:NEWP 23:NEWU60 24:NEWU8
25:NEWU9
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Listing first 45 summaries
Maximum DB seg length 15
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1 FGIFVVDKNTGDINI 15
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(1-15) from US08991628.pep
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15
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US-08-991-
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3.57e-04
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Best Local S
Matches 1
APPLICANT: STROMINGER, Jack L
APPLICANT: WUCHERFERNIG, Ka1
TITLE OF INVENTION: IDENTIFICATION OF SELF AND NON
TITLE OF INVENTION: IN AUTOIMMUNE DISEASE
FILE REFERENCE: HAR-001DV
CURRENT APPLICATION UMBER: US/08/991,628
CURRENT FILING DATE: 1997-11-15
EARLIER APPLICATION UMBER: USSN 08/400,796
EARLIER FILING DATE: 1995-03-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                               XXXXXX
                                                                                                                                                                                                                                        US-08-991-628-2
                                                                                                                                                                 Sequence 2, Application US/08991628
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                               Sequence 2, Application US/08991628 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE; 617-720-350
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO FRAGMENT TYPE: 1 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
.NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                          1 FGIFVVDKNTGDINI 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: H0498/7015WO
TELECOMMUNICATION INFORMATION:
TELECHHONE; 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 07-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF GREENFIELD &
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                    FGIFVVDKNTGDINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: GATES, EDWARD R. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
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15 AA; 1652 MW; 1115
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Y: UNITED STATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 08/400,796
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                                                                                                                                                                                                                                                                                                                                            Score 105; DB 1; Length 15; Pred. No. 3.57e-04;
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                                                                                            NON-SELF ANTIGENS IMPLICATED
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Run MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Sat May 13 05:14:06 2000; MasPar time 55.78 Seconds 3.484 Million cell updates/sec

Tabular output not generated

Description: Perfect Score: Title: Sequence: 105 1 F >US-08-991-628-2 (1-15) from US08991628.pep FGIFVVDKNTGDINI 15

Scoring table: PAM 150 Gap 15

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seq length 15

Database

a-issued 1:5A_COMB 2:5B_COMB 3:PCT_COMB 4:backfiles1

Statistics: Mean 17.421; Variance 58.153; scale 0.300

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1	Result
105	Score
105 100.0	Query Match
15	No. Score Match Length DB ID
N	Ä
US-08-400-	IJ
1 105 100.0 15 2 US-08-400- Sequence 2, Applicatio 2.01e-04	Description
icatio 2.01e-	Pred. No.
2 :	

Note: Post-processor removed 44 summaries from 119t due ៩ search parameters chosen.

ALIGNMENTS

RESULT Sequence 2, Application US/08400796 US-08-400-796-2 Sequence 2, Application US/08400796
Patent NO. 5874531
GENERAL INFORMATION:
APPLICANT: STROMINGER, JACK L.
APPLICANT: WUCHERPFENNIG, KAI
TITLE OF INVENTION: IDENTIFICAT STANDARD; IDENTIFICATION OF SELF AND NON-SELF PRT; 15 ₹

> Query Match Best Local : Matches SEQUENCE TELEFAX: . 617-720-2441
> INFORMATION FOR SEQ ID NO: Match ... 100.0%; Local Similar ty 100.0%; les 15; Conservative 1 FGIFVVDKNTGDINI 15 1 FGIFVVDKNTGDINI 15 MOLECULE TYPE: PEHYPOTHETICAL: NO FRAGMENT TYPE: in ORIGINAL SOURCE: CLASSIFICATION: 424
> ATTORNEY/AGENT INFORMATION:
> NAME: TWOMEY, MICHAEL J. SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/400,796 FILING DATE: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy TELECOMMUNICATION INFORMATION: SEQUENCE CHARACTERISTICS: LENGTH: 15 amino acids CORRESPONDENCE ADDRESS:
> ADDRESSEE: WOLF, GREENFIELD &
> STREET: 600 ATLANTIC AVENUE TITLE OF INVENTION: ANTIGENS IMPLICATED IN AUTOIMMUNE DISEASE NUMBER OF SEQUENCES: 16 TOPOLOGY: 14---STREET: CITY: B ORGANISM: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COUNTRY: U ZIP: 02210 TELEPHONE: REGISTRATION NUMBER: 38,349
> REFERENCE/DOCKET NUMBER: H0498/7015 15 AA; BOSTON ž USA HOMO SAPIENS 617-720-3500 Floppy disk internal peptide 1115 CN; Pred. Score 105; DB 2; Pred. No. 2.01e-04; 2 Mismatches SACKS, P.C. Length 15; Indels 0 Gaps 0

Search completed: Sat May 13 05:15:11 Job time : 65 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 04:40:34 2000; MasPar time 4.34 Seconds 162.858 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-991-628-2 (1-15) from US08991628.pep 105 1 FGIFVVDKNTGDINI 15

Scoring table: PAM 150 Gap 15

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seq length 15

Database:

pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 26.968; Variance 38.706; scale 0.697.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description Pred. No.

No matches found.

Search completed: Sat May 13 04:40:42 2000 Job time : 8 secs.

No matches found.	SUMMARIES Result Query No. Score Match Length DB ID Description Pre	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being pri and is derived by analysis of the total score distribution.	Statistics: Mean 27.553; Variance 34.618; scale 0.796	Database: swiss-prot38 1:swissprot	Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seq length 15	Searched: 83857 segs, 30454973 residues	Scoring table: PAM 150 Gap 15	Title: >US-08-991-628-2 Description: (1-15) from US08991628.pep Perfect Score: 105 Sequence: 1 FGIFYYDKNTGDINI 15	4.400 5111111011 6611	r time 101.68	MPsrch_pp protein - protein database search, using Smith-Waterman algorithm	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	
	• 13	ig pr							דד חלימם נפס/ ספר		aterman algorithm	Onit.	

Search completed: Sat May 13 04:35:56 2000 Job time : 112 secs.

Pred. No. is the score greater that and is derived by and is constant to the score which Level 1 and 1	Database: sptre	Searched: 225878 : Post-processing: Minimum Listing Maximum	0 0	output no	MPsrch_pp protein - Run on: Sat M	Release 3.1A John Copyright (c) 199	
No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. SUMMARIES Query Pred. No.	ptremb112 1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 1:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus ean 26.732; Variance 34.969; scale 0.764	8 seqs, 69334122 residues num Match 0% .ng first 45 summaries num DB seq length 15	5 FGIFVVDKNTGDINI 15 M 150 p 15		erman al Seconds	**************************************	

Search completed: Sat May 13 04:40:15 2000 Job time : 238 secs.

No matches found.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Run on:

Sat May 13 04:48:18 2000; MasPar time 3.03 Seconds

Run on: Sat May 13 04:48:18 2000; MasPar time 3.03 Seconds 117.095 Million cell updates/sec Tabular output not generated.

Title: >US-08-991-628-3
Description: (1-15) from US08991628.pep
Perfect Score: 96
Sequence: 1 LNSKIAFKIVSQEPA 15
Scoring table: PAM 150
Gap 15

earched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seq length 15

Database: a-geneseq35 1:geneseqp

Statistics: Mean 18.170; Variance 51.971; scale 0.350

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description Pred. No.

1 96 100.0 15 1 W04843 Self epitope of desmog 3.93e-04
2 96 100.0 15 1 W64815 Desmoglein-3 190-204. 3.93e-04
3 96 100.0 15 1 W78814 Desmoglein 3 protein f 3.93e-04

Note: Post-processor removed 42 summaries from list due to search parameters chosen

ALIGNMENTS

```
RESULT 1
ID W04843;
AC W04843;
AC W04843;
DT 18-FEB-1997 (first entry)
DE Self epitope of desmoglein 3, implicated in autoimmune disease.
KW Tolerisation; self-epitope; antigen; autoimmune disease;
KW autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte;
KW pemphigus vulgaris; desmoglein; multiple sclerosis;
KW herpes simplex virus; adenovirus; phosphomannomutase;
KW human papillomavirus; Epstein-Barr virus; DNA polymerase;
KW influenza; haemagglutinin; reovirus; sigma protein.
OS Homo sapiens.
PN W09827387-A1.
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Query Match

100.0%;

Score 96;

DB 1;

Length 15;

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PT Microparticle encapsulated nucleic acids - for recombinant
PT expression of proteins e.g. in gene therapy
PS Disclosure; Column 4; 42pp; English.

CC The patent describes a new preparation of microparticles each
CC matrix consists of one or more synthetic polymers having a solubility
CC in water of less than 1 mg/l (e.g. poly-lactic-co-glycolic acid);
CC and at least 90% of the microparticles have a diameter of less than
CC 100 microns. The microparticles are useful for the delivery of nucleic
CC acids to phagocytic cells. In one embodiment the microparticles are
CC closed circular form) includes an expression control sequence
CC operatively linked to a coding sequence, where the expression product
CC of the coding sequence is a polypeptide having a length and a sequence
CC expression product is thus an effective stimulator of an immune
CC expression product is thus an effective stimulator of an immune
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Best Local S
Matches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
US5783567-A.
21-JUL-1998.
expressed by the nucleic vulgaris.
Sequence 15 AA;
                                                         response in mammals. The prodesmoglein 3, is an example
                                                                                                                                                                                                                                                                                                                                                                                                             (PANG-) PANGAEA PHARM INC.
Curley JM, Hedley ML, Langer RS;
WPI; 98-427077/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-SEP-1998 (first entry)
Desmoglein 3 190-204.
Desmoglein DG; gene therapy; pemphigus vulgaris; microparticle;
autoantigen; autoimmune disease; MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens - useful in disease treatment, and method for identification of other self and non-self antigens implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JAN-1997; 787547.
22-JAN-1997; US-787547
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07-MAR-1996; U03182
07-MAR-1995; US-400
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(HARD ) HARVARD COLLEGE.
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Local Similarity 100.0%;
hes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; peptide;
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                              The present sequence, an antigenic portion of example of an MHC class II peptide which can be leic acid. It is associated with pemphigus
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3.93e-04;
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Search completed: Sat May 13 04:48:26 2000 Job time: 8 secs.
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                                                                                                                                                                                                                                                                         CC A microparticle preparation (MP) has been developed, consisting of CC microparticle preparation (MP) has been developed, consisting of CC (a) a polymeric matrix (PM) consisting of one or more synthetic polymers CC (a) a polymeric matrix (PM) consisting of one or more synthetic polymers CC having a solubility in water of less that 1 mg/l; and (b) an expression CC vector selected from RNA molecules (at least 50% of which are closed CC circles) or circular plasmid DNA (at least 50% of which are supercoiled). CC also described is a MP of at most 20 microns in diameter, comprising: (a) CC a PM; and (b) a NAM comprising an expression control sequence operatively CC linked to a coding sequence, where the coding sequence encodes an CC expression product selected from: (l) a polypeptide at least 7 amino CC acids in length, having a sequence identical to the sequence of: (l) a CC fragment of a naturally-occurring mammalian protein; or (il) a fragment CC a mammal; (2) a peptide having a length and sequence which permits it to bind to an MHC class I or II molecule; and (3) the polypeptide or the CC bind to an MHC class I or II molecule; and (3) the polypeptide or the CC wPS are highly effective vehicles for use in the present invention. The CC material genetic cells. They can be used for gene therapy, e.g. for CC treating genetic diseases, infections or tumours or for downregulating CC an immune response.
                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
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22-JAN-1998: UC1499.
06-JAN-1998: US-003253.
06-JAN-1997: US-787547.
22-JAN-1997: US-787547.
CURLANDER PHARM INC.
CURLANDER PHARM INC.
CURLANDER PHARM INC.
CURLANDER PHARM INC.
                                                                                                                                                                                                                                             an immune response.
Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy
Disclosure: Page 8: 101pp: English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New preparations of microparticles - comprising a synthetic polymer matrix and nucleic acid comprising an expression vector for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
W09831398-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Desmoglein 3 protein fragment 190-204.
Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen; class II associated peptide; pathogen; gene therapy; genetic disease; infection; downregulation; immune response.
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W78814;
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0; Mismatches 0;
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Pred. No. 3.
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3.93e-04
                                                                                                                                                                                                 Length 15;
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RESULT 1
ID US-08-400-796-3
XX
AC XXXXXX
DT
DT
XX
DT
CC Sequence 3, Appl
CC PAtent No. 5874
CC GENERAL INFORM
CC APPLICANT: 1
CC APPLICANT: 1
                                                                                                                                                                                                                                                                                                                     Statistics:
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Perfect Scor
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                                                                                                                                                                                                                               NO.
                                                           Sequence 3, Application US/08400796
  Sequence 3, Application US/08400796
Patent NO. 5874531
PATENT INFORMATION:
APPLICANT: STROMINGER, JACK L.
APPLICANT: WUCHERPFENNIG, KAI
                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                               Score
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                                                                                                                                                                                                 100.0
                                                                                                                                                                                                                              Match Length DB
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Listing first 45 summaries
Maximum DB seg length 15
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Gap 15
                                                                                                                                                                                                                                                                                                                     Mean 16.952; Variance 50.735; scale 0.334
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1 LNSKIAFKIVSQEPA 15
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(1-15) from US08991628.pep
                                                                                                                                                                                                                                                                                                                                                                                                          131253 seqs, 12956647 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sat May 13 05:22:51 2000;
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                                                                                                                      STANDARD;
                                                                                                                                                                              43 summaries from list due to search parameters chosen
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US-08-787-
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Sequence 24,
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2.73e-04
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RESULT
ID US
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Best Local Similarity 100.0%;
Matches 15; Conservative
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                                                                                                                                                                                                                                 Sequence 24, Application US/08787547 Patent No. 5783567
                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-720-2441 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: Per HYPOTHETICAL: NO FRAGMENT TYPE: in ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LNSKIAFKIVSQEPA 15
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
                                                                                                        CORRESPONDENCE ADDRESS
                                                          ADDRESSEE: Fish & Richardso
STREET: 225 Franklin Street
CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/400,796 FILING DATE:
              COUNTRY: US
ZIP: 02110-2804
                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                        Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. NO. _.
0; Mismatches
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Pred. No. 2.73e-04;
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Search completed: Sat May 13 05:23:57 2000 Job time: 66 secs.
                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION NUMBER: S14
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CLARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
C SEQUENCE 15 AA; 1645 MW: 1217 CN;
                                                                                                                                                             Ouery Match 100.0%; Score 96; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 2.73e-04; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                  0; Indels
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RESULT
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Sequence 24, Application US/09321346
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                                                                                               US-09-321-346-24
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Match
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Listing first 45 summaries
Maximum DB seg length 15
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Gap 15
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1:PCT 2:U6 3:U60 4:U7 5:U80 6:U81 7:U82 8:U83 9:U84A
10:U84B 11:U85 12:U86 13:U87 14:U88 15:U89 16:U90 17:U91
18:U92 19:U93 20:U94 21:U95 22:NEWP 23:NEWU60 24:NEWU8
25:NEWU9
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(1-15) from US08991628.pep
96
1 LNSKIAFKIVSQEPA 15
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US-09-003-
PCT-US96-0
US-08-991-
PCT-US98-0
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Best Local :
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APPLICANT: LUNSford, Lynn B.
APPLICANT: Putnam, David
APPLICANT: Putnam, David
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC ACID
FILE REFERENCE: 08191/014001
CURRENT APPLICATION NUMBER: US/09/321,346
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: US 09/266,463
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/09003253
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                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/09003253
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES
NUMBER OF SEQUENCES: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 24
LENGTH: 15
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application US/09321346
                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/035,98
FILING DATE: 22-2AN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Ja-
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 100.0%;
Local Similarity 100.0%;
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DUENCE 15 AA; 1645 MW;
                                                                                                                                               COMPUTER: IBM Compartible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastsEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,253
FILING DATE: 05-JAN-1998
CLASSIFICATION: 514
           REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardso
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                            STATE: MA
                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02110-2804
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                                                                                                                      60/035,983
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Pred. No. 5.13e-04;
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24:
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Best Local Similarity 100.0%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application GENERAL INFORMATION:
                                                                                                                              TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/400,796
FILING DATE: 07-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31.616
REFERENCE/DOCKET NUMBER: H0498/70:
                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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ENCE 15 AA; 1645 MW; 1217 CN;
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TYPE: ami
TOPOLOGY:
                                              ORGANISM:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                            TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                  CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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A; 1645 MW; 1217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC/TUS9603182
   Score 96; DB 1; L
Pred. No. 5.13e-04;
0; Mismatches 0
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Pred. No. 5.13e-04;
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Best Local Similarity 100.0%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/991,628
CURRENT FILING DATE: 1997-11-15
EARLIER APPLICATION NUMBER: USSN 08/400, EARLIER FILING DATE: 1995-03-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                        Sequence 24, Application PC/TUS9801499 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08991628 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: IDENTIFICATION OF SELF AND TITLE OF INVENTION: IN AUTOIMMUNE DISEASE FILE REFERENCE: HAR-001DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: STROMINGER, Jack L APPLICANT: WUCHERPFENNIG, Kai
                                                                                                                                                                                                                                                                                                                                                                          μ
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TYPE: PRT
ORGANISM: Homo sapiens
QUENCE 15 AA; 1645 MW;
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       COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/01499
FILING DATE: 22-JAN-1998
                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatik
                                                                                                                                         NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                    APPLICANT: Pangaea, Inc.
TITLE OF INVENTION: MICH
TITLE OF INVENTION: OF N
                                                                                                                                                                                                               APPLICANT:
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                                                                                                                     STREET: 225 F
CITY: Boston
STATE: MA
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                                                                                                COUNTRY: US
ZIP: 02110-2804
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Pred. No. 5.13e-04;
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Description: Perfect Score: Sequence: Result Query
No. Score Match Length DB ID Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seq length 15 Statistics: Database: Searched: Scoring table: Title: Tabular output not generated. MPsrch_pp ******************* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm PAM 150 Gap 15 pir62 1:pir1 2:pir2 3:pir3 4:pir4 >US-08-991-628-3 (1-15) from US08991628.pep 96 1 LNSKIAFKIVSQEPA 15 Sat May 13 04:47:53 2000; MasPar time 4.31 Seconds $164.283 \ \text{Million cell updates/sec}$ Mean 25.750; Variance 32.305; scale 0.797 142080 segs, 47172406 residues SUMMARIES Description Pred. No. (MT)

No matches found.

Search completed: Sat May 13 04:48:01 2000 Job time: 8 secs.

*************** (MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 04:41:28 2000: MasPar time 92.54 Seconds 4.936 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: >US-08-991-628-3 (1-15) from US08991628.pep 96 1 LNSKIAFKIVSQEPA 15

Scoring table: PAM 150 Gap 15 Sequence:

83857 seqs, 30454973 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seq length 15

swiss-prot38 l:swissprot

Database:

Statistics: Mean 26.327; Variance 28.416; scale 0.926

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID בח שם ID Description Pred. No.

No matches found.

Search completed: Sat May 13 04:43:12 2000 Job time : 104 secs.

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Result Query
No. Score Match Length DB Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seg length 15 No matches found. Statistics: Database: Searched: Scoring table: Description: Perfect Score: Tabular output not generated. Run on: MPsrch_pp Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm sptremb112
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus PAM 150 Gap 15 >US-08-991-628-3 (1-15) from US08991628.pep 96 1 LNSKIAFKIVSQEPA 15 Sat May 13 04:43:31 2000; MasPar time 228.30 Seconds 4.555 Million cell updates/sec Mean 25.549; Variance 30.093; scale 0.849 225878 segs, 69334122 residues IJ SUMMARIES Description Pred. No. (MT)

Search completed: Sat May 13 04:47:34 2000 Job time : 243 secs.

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RESULT
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AC X3
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Perfect Scor
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                                                                          US-08-991-628-4
                                                                                                                                                             Post-processor
                                                                                                                                                                                                                                                                                                                                                                     and is derived by analysis of the total score distribution
                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance score greater than or equal to the score of the result
                                                                                                                                                                                                                                                                                             Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein - protein database search, using Smith-Waterman algorithm
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Match
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Gap 15
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(1-15) from US08991628.pep
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1:PCT 2:U6 3:U60 4:U7 5:U80 6:U81 7:U82 8:U83 9:U84A
10:U84B 11:U85 12:U86 13:U87 14:U88 15:U89 16:U90 17:U91
18:U92 19:U93 20:U94 21:U95 22:NEWP 23:NEWU60 24:NEWU8
25:NEWU9
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Listing first 45 summaries
Maximum DB seg length 15
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                                                                          STANDARD;
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115
115
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PCT-US96-0
PCT-US98-0
US-09-321-
US-09-003-
US-09-187-
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Sequence 25, Applicati
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4.31e-05
4.31e-05
4.31e-05
4.31e-05
1.23e+02
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Best Local Similarity 100.0%;
Matches 15; Conservative
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TYPE: PRT
TYPE: PRT
ORGANISM: Homo sapiens
ORGANISM: 15 AA; 1722 MW; 1303 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application PC/TUS9603182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XXXXXX
                            CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/400,796
EILING DATE: 07-MR-1995
AITORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: H0498/7015
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US96-03182-4
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APPLICANT: STROMINGER, Jack L
APPLICANT: WUCHERPFENNIG, Kai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: IDENTIFICATION OF SELF AND NON-SELF ANTIGENS IMPLICATED TITLE OF INVENTION: IN AUTOIMMUNE DISEASE FILE REFERENCE: HAR-OOLDV CURRENT APPLICATION NUMBER: US/08/991,628 CURRENT FILING DATE: 1997-11-15 EARLIER FILING DATE: 1997-11-15 EARLIER FILING DATE: 1997-31-07 NUMBER: US/08/400,796 EARLIER FILING DATE: 1995-03-07 NUMBER: OF SEQ ID NOS: 20
           TELEFAX: 617-72
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TPMFLLSRNTGEVRT 15
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                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS,
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                          FILING DATE:
                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                            CITY: BOSTON
CHARACTERISTICS:
                                                                                                                                                                                                                                                                   MASSACHUSETTS
: UNITED STATES OF
                    617-720-2441
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            ID NO:
                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION OF SELF AND NON-SELF ANTIGENS IMPLICATED IN AUTOIMMUNE DISEASE
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                                                                                                                                                                      PCT/US96/03182
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Pred. No. 4.31e-05;
0; Mismatches (
           4
                                                          H0498/7015WO
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                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
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Best Local Similarity 100.0%;
Matches 15; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 15 amino acids
1 TPMFLLSRNTGEVRT 15
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                                                                                                                                                           REGISTRATION NUMBER: 34,819
REFERENCE/FOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US98/01499
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/787,547
                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish 6 Richardson, P.C
                                                             MOLECULE TYPE: peptide
ENCE 15 AA; 1722 MW; 1303 CN;
                                                                                                                                                                                        FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Jan's K.
REGISTRATION NUMBER: 34,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: PE
                                                                        TOPOLOGY: 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY TITLE OF INVENTION: OF NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fish a National Street STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
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Pred. No. 4.31e-05;
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                   Score 108; DB 1; Lo
Pred. No. 4.31e-05;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 15; Conservative
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APPLICANT: Putnam, David
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC ACII
FILE REFERENCE: 08191/014001
CURRENT APPLICATION NUMBER: US/09/321,346
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: US 09/266,463
EARLIER FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
SEQUENCE 15 AA; 1722 MW; 1303 CN;
                                                                                                                                                                                                                                                                                                                                                             XXXXXX
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                               COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                  COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                           NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: F1sh & Richardson P.C.
                                                                                                                                                                                                           APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPMFLLSRNTGEVRT
                                                                                                                                      STREET: 225 F
CITY: Boston
STATE: MA
          APPLICATION NUMBER: US/09/003,253 FILING DATE: 06-JAN-1998
CLASSIFICATION:
                                                                                                                                                               225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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Pred. No. 4.31e-05;
0; Mismatches 0
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Search completed: Sat May 13 05:39:53 2000 Job time: 408 secs.
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GENERAL INFORMATION:
GAPPLICANT: Blaschuk, Orest W.
APPLICANT: GOUX, BARDAYA J.
CHAPTICANT: GOUX, BARDAYA J.
CHAPTICANT: GOUX, CAMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL TITLE OF INVENTION: CAMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL CITLE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859
CURRENT FILING DATE: 1998-11-06
CURRENT FILING DATE: 19
                                                                                                                                                                                                                                                                                                                                         Query Match 54.6%;
Best Local Similarity 70.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 15; Conservative
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APPLICATION NUMBER: 60/035,983
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fraser Ph.D. J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8006
TELEFAX: 617/542-8006
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 15 AA; 1722 MW; 1303 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: Desmoglein cell adhesion recognition sequence
SEQUENCE 11 AA; 1323 MW; 536 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XXXXXX
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                                                                                                                                                                                                                     2 MFIINRNTGE 11
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                                                                                                                                                                                                                                                                                                                                         Score 59; DB 17; Length 11; Pred. No. 1.23e+02; 3; Mismatches 0; Indels
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 04:53:44 2000; MasPar time 4.32 Seconds 163.716 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-991-628-4 (1-15) from US08991628.pep 108 1 TPMFLLSRNTGEVRT 15

Scoring table: PAM 150 Gap 15

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seq length 15

Database:

pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 27.219; Variance 35.537; scale 0.766

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID

Description

Pred. No.

Search completed: Sat May 13 04:53:53 2000 Job time: 9 secs.

No matches found.

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matches found.	SUMMARIES Result Query No. Score Match Length DB ID Description	<pre>Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score</pre>	Statistics: Mean 27.727; Variance 32.559; sca	Database: swiss-prot38 1:swissprot	Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seq length 15	Searched: 83857 seqs, 30454973 residues	Scoring table: PAM 150 Gap 15	Title: >US-08-991-628-4 Description: (1-15) from US08991628.pep Perfect Score: 108 Sequence: 1 TPMFLLSRNTGEVRT 15	Tabular output not generated.	Run on: Sat May 13 04:48:45 2000; MasPar t:	MPsrch_pp protein - protein database search, using	Release 3.1A John F. Collins, Biocomputing Copyright (c) 1993–1998 University of Edir Distribution rights by Oxford Molec	
	cription Pred. No.	cted by chance to have a of the result being printed, score distribution.	scale 0.852							Par time 90.27 Seconds	search, using Smith-Waterman algorithm	Biocomputing Research Unit. ersity of Edinburgh, U.K. V Oxford Molecular Ltd	

Search completed: Sat May 13 04:50:23 2000 Job time: 98 secs.

Statistics: Mean 27.384; V. Pred. No. is the number of score greater than or equa and is derived by analysis	Database: sptrembll2 1:sp_archea 5:sp_invert. 9:sp_phage: 13:sp_vertel	Post-processing: Minimum Mar Listing fi Maximum DB		Scoring table: PAM 150	Title: >US-08-991-628-4 Description: (1-15) from US089 Perfect Score: 108 Sequence: 1 TPMFLLSRNTGEVRT	Tabular output not generated	Run on: Sat May 13	MPsrch_pp protein - prote	**************************************	
84; Variance 31.843; scale 0.860 ber of results predicted by chance to have a r equal to the score of the result being printed, alysis of the total score distribution.	trembil2 1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus	Match 0% first 45 summaries DB seg length 15	gs, 69334122 residues		1-628-4 om US08991628.pep RNTGEVRT 15		May 13 04:50:42 2000; MasPar time 149.09 Seconds	protein database search, using Smith-Waterman algorithm	**************************************	[Tw)

Description

Result Query
No. Score Match Length DB ID

SUMMARIES

Pred. No.

No matches found.

Search completed: Sat May 13 04:53:24 2000 Job time: 162 secs.

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Page 1

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MPsrch_pp protein - protein database search, using Smith-Waterman

Run on: Sat May 13 04:59:02 2000; MasPar time 3.04 Seconds 116.885 Million cell updates/sec

Tabular output not generated

Description: Perfect Score: 113 1 C >US-08-991-628-5 (1-15) from US08991628.pep

CECNIKVKDVNDNFP 15

Scoring table: PAM 150 Gap 15 Sequence:

188963 segs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seq length 15

Database: a-geneseg35 1:geneseqp

Statistics: Mean 18.468; Variance 59.453; scale 0.311

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult Query No. Score Match Length DB ID Description Pred. No. 1 113 100.0 15 1 W04845 Self epitope of desmog 3.35e-05 2 52 46.0 11 1 W13139 Human cadherin-5 antig 1.72e+02
Query Query Match Length DB ID Description Pred. No. 100.0 15 1 W04845 Self epitope of desmog 3.35e-05 46.0 11 1 W13139 Human cadherin-5 antig 1.72e+02
Length DB ID Description Pred. No. 15 1 W04845 Self epitope of desmog 3.35e-05 11 1 W13139 Human cadherin-5 antig 1.72e+02
DB ID Description Pred. No. 1 W04845 Self epitope of desmog 3.35e-05 1 W13139 Human cadherin-5 antig 1.72e+02
ID Description Pred. No. W04845 Self epitope of desmog 3.35e-05 W13139 Human cadherin-5 antig 1.72e+02
Description Pred. No. Self epitope of desmog 3.35e-05 Human cadherin-5 antig 1.72e+02
Pred. No. 09 3.35e-05

Note: Post-processor removed 43 summaries from list due 6 search parameters

ALIGNMENTS

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PPOKKKKKKETC
Homo sapiens.
W09627387-A1.
12-SEP-1996.
                                                    18-FEB-1997 (first entry)
Self epitope of desmoglein 3, implicated in autoimmune disease.
Tolerisation; self-epitope; antigen; autoimmune disease;
autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte;
pemphigus vulgaris; desmoglein; multiple sclerosis;
herpes simplex virus; adenovirus; phosphomannomutase;
human papillomavirus; Epstein-Barr virus; DNA polymerase;
influenza; haemagglutinin; reovirus; sigma protein.
                                                                                                                                                                                                                       W04845 standard; peptide; 15 AA.
W04845;
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Search completed: Sat May 13 04:59:09 2000 Job time: 7 secs.

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                                                               Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 1
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17-APR-1992; 872643.
17-APR-1992; US-872643.
19-APR-1993; US-049460.
26-JAN-1994; US-188228.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cadherin-5 antigenic epitope (residues 242-252). Ca2+ dependent; cell adhesion protein; cadherin; human; antibody; purification; determination; epitope; tissue expression; binding antagonist; calcium ion; antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HARD ) HARVARD COLLEGE.
Strominger JL, Wucherpfennig
WPI: 96-425218/42.
                                                                                                                                 Sequence
                                                                                                                                               Claim 5; Column 112; 59pp; English.
The present sequence is an antigenic epitope from human cadherin-5, which is a Ca2+ dependent cell adhesion protein. Antibodies or fragments that specifically bind the epitope can be used to purify the cadherin, determine its tissue expression and antagonise its ligand/antiligand binding activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W13139 standard; Protein; 11 AA. W13139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens - useful in disease treatment, and method for identification of other self and non-self antigens implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-1996; U03182.
07-MAR-1995; US-400796.
                                                                                                                                 ligand/antiligand
Sequence 11 AA;
                                                                                                                                                                                                                                                                  Antibodies to
                                                                                                                                                                                                                                                                                                 Suzuki
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                               1 VTLQDINDNFP 11
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 IKVKDVNDNFP
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Similarity 100.0%;
15; Conservative
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                                                               46.0%;
larity 54.5%;
Conservative
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                                                                                                                                                                                                                                                               cadherin proteins - useful
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                                                               Score 52; DB 1; 1
Pred. No. 1.72e+02;
3; Mismatches
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Pred. No. 3.35e-05;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                  cadherin
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                                                                                                Length 11;
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                                                                                                                                                                                                                human cadherin-5,
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Release Copyrig	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	
۹Psrch_pp protein Nun on: Sa	protein database searct May 13 05:40:13 2000;	
ular output no	generated.	
Pitle: Description: Derfect Score: Sequence:	>US-08-991-628-5 (1-15) from US08991628.pep 113 1 CECNIKVKDVNDNFP 15	
scoring table:	PAM 150 Gap 15	
earched:	131253 segs, 12956647 residues	
ost-processing:	Minimum Match 0% Listing first 45 summaries Maximum DB seq length 15	
Database:	a-issued 1:5A_COMB 2:5B_COMB 3:PCT_COMB 4:backfiles1	
Statistics:	Mean 17.500; Variance 58.000; scale 0.302	
Pred. No. is the score greater that and is derived	is the number of results predicted by chance to have a ter than or equal to the score of the result being printed, ived by analysis of the total score distribution.	
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ult No. Score	ery tch Length DB ID Description I	
1 113	15 2 US-08-400- Sequence	
Note: Post-processor	ssor removed 44 summaries from list due to search parameters chosen. ALIGNMENTS	
RESULT 1 ID US-08-400-796	96-5 STANDARD; PRT; 15 AA.	
CX XXXXX		
Sequence 5,	Application US/08400796	
Sequence 5 Patent No. GENERAL I	, Application US/08400796 5874531 NFORMATION:	
	F INVENTION: IDENTIFICATION OF SELF AND NON-SELF	

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Search completed: Sat May 13 05:41:15 2000 Job time : 62 secs.
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ANTIGENS IMPLICATED IN AUTOIMMUNE DISEASE

NUMBES OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSE: MOLF, GREENVIELD & SACKS, P.C.

STATE: MA

COUVITY: BOSTON

STATE: MA

COUVITY: BOSTON

STATE: MA

COUVITY: UGA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIC Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/400,796

FILING DATE:

CLASSIFICATION NUMBER: US/08/400,796

FILING DATE:

APPLICATION NUMBER: US/08/400,796

FILEDHONE: A1-710-104

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 38,349

REFERENCE/DOCKET NUMBER: 10498/7015

TELEPHONE: 617-720-3500

TELEPHONE: 617-720-3500

TELEPHONE: 617-720-3500

TELEPHONE: 617-720-3500

TELEPHONE: A1-720-3500

TELEPHONE: A1-720-3500

TELEPHONE: A1-720-3500

TELEPHONE: 15 amino acids

TYPE: amino acids

TOPOLOGY: Tinear

COMPARENT TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: amino acids

TOPOLOGY: Allerinal

ORGANISM: HOMO SAPIENS

ORGANISM: HOMO SAPIENS

ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
                                                                                                                             Score 113; DB 2; Length 15; Pred. No. 2.27e-05; 0; Mismatches 0; Indels
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Result
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Perfect Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein - protein database search, using
                                                                                                                                                                                                                                          greater than or equal to the score of the result bein derived by analysis of the total score distribution.
                             5, Application PC/TUS9603182
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Match
  5, Application PC/TUS9603182
INFORMATION:
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1:PCT 2:U6 3:U60 4:U7 5:U80 6:U81 7:U82 8:U83 9:U84A

10:U84B 11:U85 12:U86 13:U87 14:U88 15:U89 16:U90 17:U91

18:U92 19:U93 20:U94 21:U95 22:NEWP 23:NEWU60 24:NEWU8

25:NEWU9
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Gap 15
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US-08-991-
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                                                                                                                  ALIGNMENTS
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Applicatio
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
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TITLE OF INVENTION: IDENTIFICATION: ANTIGENS IMPLICATION: ANTIGENS IMPLICATION: ANTIGENS INPLICATION: ANTIGENSES:
ADDRESSEE: WOLF, GREENFIELD & SAADDRESSEE: WOLF, GREENFIELD & WOLF, GREENFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08991628 GENERAL INFORMATION:
APPLICANT: STRONLINGER, Jack L APPLICANT: WUCHERPFENNIG, Kai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 61/-/-
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE 15 amino acids
                         TITLE OF INVENTION: IDENTIFICATION OF SELF TITLE OF INVENTION: IN AUTOIMMUNE DISEASE FILE REFERNCE: HAR-001DV CURRENT APPLICATION NUMBER: US/08/991,628 CURRENT FILING DATE: 1997-11-15 EARLIER APPLICATION NUMBER: USSN 08/400,79 EARLIER FILING DATE: 1995-03-07 NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 07-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CECNIKVKDVNDNFP 15
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CECNIKVKDVNDNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 AA; 1738 MW; 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08991628
PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MASSACHUSETTS
: UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION OF SELF AND NON-SELF ANTIGENS IMPLICATED IN AUTOIMMUNE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٠..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 113; DB 1; Pred. No. 1.48e-05;
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                                                                                                         08/400,796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.25
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                                                                                                                                                                                                                                                                                AND NON-SELF ANTIGENS IMPLICATED
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(MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 04:58:36 2000; MasPar time 4.28 Seconds 165.342 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-08-991-628-5 (1-15) from US08991628.pep 113

Sequence: 1 CECNIKVKDVNDNFP 15

Scoring table: PAM 150 Gap 15

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seq length 15

pir62 1:pir1 2:pir2 3:pir3 4:pir4

Database:

Statistics: Mean 25.922; Variance 35.935; scale 0.721

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB Ħ Description Pred. No.

No matches found.

Search completed: Sat May 13 04:58:44 2000 Job time: 8 secs.

Search completed: Sat May 13 04:56:06 2000 Job time : 89 secs.

No matches found.

Result No. Score	18 9 N	Statistics:	Database:	Post-processing:	Searched:	Scoring table:	Title: Description: Perfect Score: Sequence:	Tabular output	Run on:	MPsrch_pp pro		
SUMMARIES Query Match Length DB ID	e number c han or equ by analysi	Mean 25.749; Variance	<pre>sptrembl12 1:sp_archea 2:sp_bacteria 5:sp_invertebrate 6:sp_mai 9:sp_phage 10:sp_plant 11 13:sp_vertebrate 14:sp_vi</pre>	: Minimum Match 0% Listing first 45 summaries Maximum DB seq length 15	225878 segs, 69334122	PAM 150 Gap 15	>US-08-991-628-5 (1-15) from US08991628. 113 1 CECNIKVKDVNDNFP 15	not generated.	Sat May 13 04:56:23 2000;	protein - protein database :	Release 3.1A John F. Collins, Biocomputing Rese Copyright (c) 1993-1998 University of Edinburg Distribution rights by Oxford Molecular	
IES Description	s predicted by chance e score of the result total score distribu	32.815; scale 0.785	3:sp_fung: nmal 7:sp_r :sp_rodent rus	ries 15	residues		. pep	3.025 MILLION COLL	MasPar time 10	search, using Smith-Waterman	llins, Biocomputing Research University of Edinburgh, U. ghts by Oxford Molecular Ltd	
Pred. No.	to have a being printed, tion.		<pre>l 4:sp_human nhc 8:sp_organelle 12:sp_unclassified</pre>					ד חליחם רבים/ סבר	Seconds	terman algorithm		* *

Search completed: Sat May 13 04:58:17 2000 Job time: 114 secs.

No matches found.

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07-MAR-1996; U03182.

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                                                                                                                                                                                           PR (HARD ) HARVARD COLLEGE.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Wucherpfennig KW;

DR WPI; 96-425218/42.

Premphigus vulgaris auto-antigens and multiple sclerosis non-self prince antigens - useful in disease treatment, and method for prince indentification of other self and non-self antigens implicated in pridentification of other self and non-self antigens implicated in pridentification preparations for tolerisation to antigens comprise cliher an isolated human non-collagen or non-myslin basic protein companies of tolerising an individual to an autoantigen; or an isolated human pathogen polypeptide capable of tolerising an individual to that polypeptide. In both cases, the compressing an individual to that polypeptide. In both cases, the colypeptide (whether self or non-self) includes an amino acid sequence corresponding to a sequence motif for a MHC class II protein, such as HLA-DR, which is associated with a human autoimmune colleges and which binds to the polypeptide to activate autoreactive corresponded in human desmoglein 3 protein cated is implicated as a self epitope in pemphigus vulgaris. Peptide is companied from the human desmoglein protein are described in W04841-47.

So sequence 15 AA;
                                                                                                 Query Match 100.0%; Score 109; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 5.72e-05; Matches 15; Conservative 0; Mismatches 0; Indels
                          1 SARTLNNRYTGPYTF 15
  1 SARTLNNRYTGPYTF 15
                                                                                                    0;
                                                                                                 Gaps
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Search completed: Sat May 13 05:06:15 2000 Job time: 7 secs.

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RESULT 1
ID US-08-400-796-6
XX
AC XXXXXX
AC XXXXXX
DT
XX
DT
XX
CC Sequence 6, Appli
CC Sequence 6, Appli
CC Patent No. 58745
CC GENERAL INFORMA
CC APPLICANT: %
CC APPLICANT: %
CC APPLICANT: WITH A PROBLEM APPLICANT APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
No.
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description:
Perfect Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Statistics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tabular output not generated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: Post-processor removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPsrch_pp
                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08400796
    Sequence 6, Application US/08400796
Patent No. 5874531
GENERAL INFORMATION:
APPLICANT: STROMINGER, JACK L.
APPLICANT: WUCHERPFENNIG, KAI
TITLE OF INVENTION: IDENTIFICATION OF SELF AND NON-SELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein - protein database search, using Smith-Waterman algorithm
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Match Length DB
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Gap 15
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(1-15) from US08991628.pep
109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mean 18.236; Variance 59.295; scale 0.308
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1:5A_COMB 2:5B_COMB 3:PCT_COMB 4:backfiles1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sat May 13 05:49:00 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 summaries from list due to search parameters chosen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Applicatio 7.06e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
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Search completed: Sat May 13 05:50:03 2000 Job time : 63 secs.
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                                                                         В
                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                     TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                         1 SARTLNNRYTGPYTF 15
                                                  1 SARTLNNRYTGPYTF
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY, MICHAEL J.
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: ANTIGENS IMPLICATED IN AUTOIMMUNE DISEASE NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: ADDRESS: WOLF, GREENFIELD & SACKS, P.C.
                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                              MOLECULE TYPE: PHYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 38,349
REFERENCE/DOCKET NUMBER: HO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: WC
STREET: 600 A
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/400,796 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UP
                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
                                                                                                                                               15 AA; 1761 MW; 1506 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: WOLF, GREENFIELD 600 ATLANTIC AVENUE
                                                                                                                                                             HOMO SAPIENS
                                                                                                                                                                                   internal
                                                                                                                                                                                                        peptide
                                                                                               Score 109; DB 2; Le
Pred. No. 7.06e-05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                       <u>ه</u>
                                                                                                                                                                                                                                                                                                                      H0498/7015
                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.
                                                                                                                        Length 15;
                                                                                                   Indels
                                                                                                 0
                                                                                                 Gaps
```

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 05:50:23 2000; MasPar time 402.79 Seconds 4.157 Million cell updates/sec

Tabular output not generated

Description: Perfect Score: >US-08-991-628-6 (1-15) from US08991628.pep

Sequence: 109 1 S SARTLNNRYTGPYTF 15

Scoring table: PAM 150 Gap 15

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

714217 seqs, 111628056 residues

Maximum DB seg length 15

a-pending 1:PCT 2:U6 3:U60 4:U7 5:U80 6:U81 7:U82 8:U83 9:U84A 10:U84B 11:U85 12:U86 13:U87 14:U88 15:U89 16:U90 17:U91 18:U92 19:U93 20:U94 21:U95 22:NEWP 23:NEWU60 24:NEWU8 25:NEWU9

Statistics: Mean 21.442; Variance 54.363; scale 0.394

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution

SUMMARIES

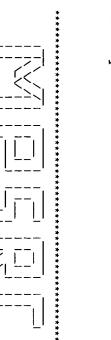
Pred. No. Score Match Length DB ID Description Pred. No. No. No. No. No. No. No. No. No. No	ω 22 L	Result No.
Ouery Match Length DB ID Match L	109 109 56	Score
Length DB ID Description Pred. No. 15 1 PCT-US96-0 Sequence 6, Applicatio 2.15e-05 15 15 US-08-991 Sequence 6, Applicatio 2.15e-05 10 19 US-09-361- Sequence 6, Applicatio 2.19e+02	100.0	Query Match
PCT-US96-0 Sequence 6, Applicatio 2.15e-05 US-08-991- Sequence 6, Applicatio 2.15e-05 US-08-9361- Sequence 6, Applicatio 2.19e+02	15 15 16 10 19	Length DE
Description Pred. No.	PCT-US96-0 US-08-991- US-09-361-	ib
Applicatio 2.15e-05, Applicatio 2.15e-05, Applicatio 2.15e-05, Applicatio 2.19e+02	Sequence 6 Sequence 6	Descriptio
Pred. No. 2.15e-05 2.15e-05 2.19e+02	, Applicatio , Applicatio , Applicatio	n
	2.15e-05 2.15e-05 2.19e+02	Pred. No.

Note: Post-processor removed 42 summaries from list due to search parameters chosen

ALIGNMENTS

RESULT
XX
AC
XX
DT
DT
CCC
XX
XX
XX Sequence 6, Application PC/TUS9603182 XXXXXX PCT-US96-03182-6 Sequence Ó Application STANDARD; PC/TUS9603182 PRT; 15 ₿

Ş 밁 RESULT Query Match 100.0%; Score Best Local Similarity 100.0%; Pred. Matches 15; Conservative 0;) Sequence 6, Application US/08991628,
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: STROMINGER, Jack L
APPLICANT: WUCHERPFENNIG, Kai
TITLE OF INVENTION: IDENTIFICATION OF SELF AND
TITLE OF INVENTION: IN AUTOIMMUNE DISEASE
FILE REFERENCE: HAR-OOLDV
CURRENT APPLICATION NUMBER: US/08/991,628
CURRENT FILING DATE: 1997-11-15
EARLIER APPLICATION NUMBER: USSN 08/400,796
EARLIER FILING DATE: 1995-03-07
NUMBER OF SEQ ID NOS: 20 SEQUENCE Sequence 6, Application US/08991628 US-08-991-628-6 CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/400,796
APPLICATION NUMBER: US 08/400,796
FILING DATE: 07-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: H0498/7015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500 TELEFAX: 617-720-2441 INFORMATION FOR SEQ ID NO: GENERAL INFORMATION: APPLICANT: س 1 SARTLNNRYTGPYTF 15 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE FRAGMENT TYPE: ORIGINAL SOURCE: SEQUENCE CHARACTERISTICS: LENGTH: 15 amino acids TITLE OF INVENTION: MOLECULE TYPE: SARTLNNRYTGPYTF 15 STREET: 600 A CITY: BOSTON STATE: MASSAC ORGANISM: H COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS APPLICATION NUMBER: FILING DATE: COUNTRY: TOPOLOGY: linear amino acid MASSACHUSETTS
UNITED STATES OF AMERICA HOMO SAPIENS 1; 1761 MW; 1506 CN; STANDARD; internal peptide IDENTIFICATION OF SELF AND NON-SELF ANTIGENS IMPLICATED IN AUTOIMMUNE D Score 109; DB 1; Leux PCT/US96/03182 6: H0498/7015WO 15 ξ AND Length 15 NON-SELF ANTIGENS IMPLICATED Indels 0 DISEASE Gaps 0,



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(MT)

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 05:05:40 2000; MasPar time 4.33 Seconds 163.439 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score: >US-08-991-628-6 (1-15) from US08991628.pep 109 1 SARTLNNRYTGPYTF 15

Scoring table: PAM 150 Gap 15

Sequence:

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seg length 15

Database:

pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 26.736; Variance 36.896; scale 0.725

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.

Result Query
No. Score Match Length DB ij Description

Search completed: Sat May 13 05:05:49 2000 Job time: 9 secs.

No matches found.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 04:59:27 2000; MasPar time 83.07 Seconds 5.499 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-991-628-6 (1-15) from US08991628.pep 109 1 SARTLNNRYTGPYTF 15

Scoring table: PAM 150 Gap 15

Searched: 83857 segs, 30454973 residues

Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seq length 15

swiss-prot38 1:swissprot

Database:

Statistics: Mean 27.244; Variance 33.691; scale 0.809

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description Pred. No.

No matches found.

Search completed: Sat May 13 05:01:04 2000 Job time: 97 secs.

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Statistics: Database: Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seg length 15 Searched: Scoring table: Sequence: Description: Perfect Score: Tabular output not generated. Run on: MPsrch_pp .protein - protein database search, using Smith-Waterman algorithm Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd PAM 150 Gap 15 sptremb112
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
1:sp_archea 2:sp_bacteria 7:sp_mhc 8:sp_organelle
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_bage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus >US-08-991-628-6 (1-15) from US08991628.pep 109 1 SARTLNNRYTGPYTF 15 Sat May 13 05:01:23 2000; MasPar time 224.41 Seconds
4.634 Million cell updates/sec Mean 26.282; Variance 35.962; scale 0.731 225878 segs, 69334122 residues *****************

Result Query
No. Score Match Length DB Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

No matches found

H

Description

Pred. No

Search completed: Sat May 13 05:05:22 2000 Job time: 239 secs.

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RESULT 1 1 W04847 standard; peptide; 15 AA. AC w04847; AC w04847; DT 18-FEB-1997 (first entry) DT 18-EB-1997 (first entry) DE Self epitope of desmoglein 3, implicated in autoimmune disease. KW Tolerisation; self-epitope; antigen; autoimmune disease; KW autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte; KW pemphigus vulgaris; desmoglein; multiple sclerosis; KW herpes simplex virus; adenovirus; phosphomannomutase; KW human papillomavirus; Epstein-Barr virus; DNA polymerase; KW influenza; haemagglutinin; reovirus; sigma protein. DN w09627387-A1. DD 12-SEP-1996; U03182.	ALIGNMENTS	Note: Post-processor removed 44 summaries from list due to search parameters chosen	Result Query No. Score Match Length DB ID Description Pred. No. 1 99 100.0 15 1 W04847 Self epitope of desmog 5.70e-04	SUMMARIES	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Statistics: Mean 17.183; Variance 54.742; scale 0.314	Database: a-geneseq35 1:geneseqp	Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seg length 15	Searched: 188963 seqs, 23686106 residues	Scoring table: PAM 150 Gap 15	Title: >US-08-991-628-7 Description: (1-15) from US08991628.pep Perfect Score: 99 Sequence: 1 QSGTMRTRHSTGGTN 15	Tabular output not generated.	Λ.	MPsrch_pp protein - protein database search, using Smith-Waterman algorithm	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	(HR)	***************************************
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PA (HARD ) HARVARD COLLEGE.

PA (HARD ) HARVARD COLLEGE.

PR Strominger JL, wucherpfennig KW;

DR WPI; 96-425218/42.

Pr emphigus vulgaris auto-antigens and multiple sclerosis non-self printification of other self and non-self antigens implicated in pridentification of other self and non-self antigens implicated in Pr auto-immune disease

PS Claim 1; Page 42; 58pp; English.

CC Pharmaceutical preparations for tolerisation to antigens comprise claim 1; Page 42; 58pp; English.

CC Pitter an isolated human non-collagen or non-myslin basic protein clather an isolated human pathogen polypeptide capable of tolerising an individual to that polypeptide. In both cases, the CC sequence corresponding to a sequence motif for a MHC class II correction, such as HLA-DR, which is associated with a human autoimmune colsease and which binds to the polypeptide to activate autoreactive correctles in individuals with the autoimmune disease. This peptide is conditived from the human desmoglein 3 protein carids 762-786; and is implicated as self epitope in pemphigus vulgaris. Peptides corrected from the human desmoglein protein are described in W04841-47.
                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
1 QSGTMRTRHSTGGTN 15
||||||||||||||
1 QSGTMRTRHSTGGTN 15
                                                                                          Score 99; DB 1; Length 15; Pred. No. 5.70e-04; 0; Mismatches 0; Indels
                                                                                               0; Indels
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                                                                                          Gaps
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Search completed: Sat May 13 05:13:48 Job time : 7 secs.

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Result
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Perfect Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
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                                                                                                                                                                                                                         US-08-400-796-7
                                                                                                                     Sequence 7, Application US/08400796
                                                                                                                                                                                         XXXXXX
                                                    Sequence 7, Application US/08400796
Patent No. 5874531
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                          Query
Score Match Length DB ID
APPLICANT: STROMINGER, JACK L.
APPLICANT: WUCHERPFENNIG, KAI
TITLE OF INVENTION: IDENTIFICATION OF SELF AND NON-SELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
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Gap 15
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1:5A_COMB 2:5B_COMB 3:PCT_COMB 4:backfiles1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum Match 0%
Listing first 45 summaries
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(1-15) from US08991628.pep
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mean 16.273; Variance 51.318; scale 0.317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sat May 13 05:57:42 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maximum DB seq length 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131253 segs, 12956647 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QSGTMRTRHSTGGTN 15
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4.120 Million cell updates/sec
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                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
                                                                                                SEQUENCE
                                                                                                                                                                                                                     TELEFAX: 617-720-2441 TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,796
FILING DATE:
FILING DATE:
                                                                                             MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
EQUENCE 15 AA; 1591 MW; 1253
               1 QSGTMRTRHSTGGTN 15
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                REGISTRATION NUMBER: 38,349
REFERENCE/DOCKET NUMBER: HO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY, MICHAEL J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ANTIGENS IMPLICATED IN AUTOIMMUNE DISEASE NUMBER OF SEQUENCES: 16
                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 600 CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 02210
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: WOLF, GREENFIELD & SACKS, P.C. 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                 1253 CN;
                                                            Score 99; DB 2;
Pred. No. 1.89e-04
                                                                                                                                                                                                                                                                      H0498/7015
                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
                                                                        Length 15;
                                                 Indels
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                                                Gaps
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Search completed: Sat May 13 05:58:40 2000 Job time : 58 secs.

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RESULT RESULT PO
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No.
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Perfect Score:
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                                                                                                                                             Note: Post-processor removed 43 summaries from list due to search parameters chosen.
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                                                                   XXXXXX
                                                                                     PCT-US96-03182-7
                            Sequence 7, Application PC/TUS9603182
Sequence 7, Application PC/TUS9603182 GENERAL INFORMATION:
                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein - protein database search, using Smith-Waterman algorithm
                                                                                                                                                                                          Query
Match Length DB
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Listing first 45 summaries
Maximum DB seg length 15
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Gap 15
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                                                                                                                                                                                                                                                                                                  a-pending
1:PCT 2:U6 3:U60 4:U7 5:U80 6:U81 7:U82 8:U83 9:U84A
10:U84B 11:U85 12:U86 13:U87 14:U88 15:U89 16:U90 17:U91
18:U92 19:U93 20:U94 21:U95 22:NEWP 23:NEWU60 24:NEWU8
25:NEWU9
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(1-15) from US08991628.pep
                                                                                                                                                                                                                                                                                Mean 19.349;
                                                                                                                                                                                                                                                                                                                                                                                                  714217 segs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSGTMRTRHSTGGTN 15
                                                                                                                                                                 15
15
                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                   111628056 residues
                                                                                                                                                                                                                                                                                Variance 49.952;
                                                                                                                                                                PCT-US96-0
US-08-991-
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                                                                                                                  ALIGNMENTS
                                                                                                                                                                                     [D Description
                                                                                                                                                                                                                          SUMMARIES
                                                                                      PRT;
                                                                                                                                                               Sequence 7, Sequence 7,
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                                                                                                                                                                                                                                                                               scale 0.387
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Applicatio
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1.97e-04
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                  XXXXXX
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US-08-991-628-7
                                                                                                                                                                                                                                        Sequence 7, Application US/08991628
                                                                                                                                                                                 Sequence 7, Application US/08991628 GENERAL INFORMATION:
APPLICANT: STROMINGER, Jack L
APPLICANT: WICHERFERNIG, Kai
TITLE OF INVENTION: IDENTIFICATION OF SELF AND NON-SELF ANTIGENS IMPLICATED
TITLE OF INVENTION: IN AUTOIMMUNE DISEASE
FILE REFERENCE: HAR-001DV
CURRENT APPLICATION NUMBER: US/08/991,628
CURRENT FILING DATE: 1997-11-15
CURRENT FILING DATE: 1997-11-15
EARLIER FILING DATE: 1995-03-07
NUMBER OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QSGTMRTRHSTGGTN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: GATES, EDWARD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GRENFIELD
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                          QSGTMRTRHSTGGTN 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: GATES, EDWARD R. REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/400,796 FILING DATE: 07-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA; 1591 MW; 1253 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT/US96/03182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 99; DB 1;
Pred. No. 1.97e-04
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SOFTWARE:

PatentIn

SEQ ID NO 7 LENGTH: 15 TYPE: PRT TYPE: PRT ORGANISM: Homo sapiens SEQUENCE 15 AA: 1591 MW: 1253 CN: SEQUENCE 15 AA: 1591 MW: 15	Sear Job	Оy	Be. Ma	ននននន
	Search completed: Sat May 13 06:05:57 2000 Job time : 415 secs.	1 OSGTMRTRHSTGGTN 15 	; Score 99; DB 15; Length 15; ; Pred. No. 1.97e-04; 0; Mismatches 0; Indels 0; Gaps	SEQUENCE 15 AA; 1591 MW; 1253 CN;

(MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 05:13:15 2000; MasPar time 4.30 Seconds 164.392 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-991-628-7 (1-15) from US08991628.pep 99 1 QSGTMRTRHSTGGTN 15

Scoring table: PAM 150 Gap 15

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seg length 15

Database:

1:pirl 2:pir2 3:pir3 4:pir4

Statistics: Mean 23.943; Variance 29.203; scale 0.820

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB

IJ Description

Pred. No.

No matches found.

Search completed: Sat May 13 05:13:24 2000 Job time : 9 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 05:06:34 2000; MasPar time 91.30 Seconds 5.004 Million cell updates/sec

Tabular output not generated.

Sequence: Description: Perfect Score: >US-08-991-628-7 (1-15) from US08991628.pep 99 1 QSGTMRTRHSTGGTN 15

Scoring table: PAM 150 Gap 15

Searched: 83857 segs, 30454973 residues

Post-processing: Minimum Match 0% Listing first 45 summaries Maximum DB seg length 15

swiss-prot38 l:swissprot

Database:

Statistics: Mean 24.519; Variance 27.183; scale 0.902

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID

Description

Pred. No.

Search completed: Sat May 13 05:08:16 2000 Job time : 102 secs.

No matches found.

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Releas Copyri	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
MPsrch_pp protein	ein - protein database search, using Smith-Waterman algorithm.
Run on: Tabular output n	Sat May 13 05:08:36 2000; MasPar time 245.94 Seconds ont generated.
Title: Description:	>US-08-991-628-7 (1-15)
Perfect Score: Sequence:	99 1 QSGTMRTRHSTGGTN 15
Scoring table:	PAM 150 Gap 15
Searched:	225878 seqs, 69334122 residues
Post-processing:	Minimum Match 0% Listing first 45 summaries Maximum DB seq length 15
Database:	<pre>sptremb112 1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus</pre>
Statistics:	Mean 24.224; Variance 25.706; scale 0.942
Pred. No. score great and is der	No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
	8 SUMMARIES
Result Qu	Query Match Length DB ID Description Pred. No.
No matches found	

Search completed: Sat May 13 05:12:56 2000 Job time : 260 secs.



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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Sat May 13 07:05:15 2000; MasPar time 3.02 Seconds $117.657 \ \text{Million cell updates/sec}$

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-991-628-2 (1-15) from US08991628.pep 105

1 FGIFVVDKNTGDINI 15

Scoring table: PAM 150 Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 18.538; Variance 60.235; scale 0.308

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	22	21	20	19	18	. 17	16	15	14	13	12	11	10	9	8	7	6	Ç	4	w	2	1	NO.	Result
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sp.	S		Arabidopsis chloroplas	eceptor p	\sim	Full length human cadh	Cadherin-11.	Sequence encoded by mu	dherin-11	encoded by	encoded by	GHPC	ORF	H. pylori ORF hp7e1043	Ŧ	•	ombinir	Peptide combining with	phigus	rig	ining wit	Self epitope of desmog	Description	
٠	7.45e+01	٠.	7.45e+01	:_	:-		:~	:_	٠		5.92e+01	'n	٠	5.92e+01	1.36e-01	8.20e-02	_	_	3.51e-04	4.3		.51e-	Pred. No.	

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1 FGIFVVDKNTGDINI 15 ||||||||||||||| 1 FGIFVVDKNTGDINI 15

Query Match 100.0%; Best Local Similarity 100.0%; Matches 15; Conservative

Score 105; DB 1; Length 15; Pred. No. 3.51e-04; 0; Mismatches 0; Indels

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Gaps

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O.	Product of alternative	Protocadherin clone 42	Human protocadherin-42	9	Malassezia fungus MF-5	Streptococcus pneumoni	Human filamin.	Putative human cadheri	Human cadherin-12.	Helicobacter pylori ur	_	rheae pilC2	Sequence encoded by th	Human hSI protein sequ	Human E-cadherin precu	Sequence of human live	Tobamovirus replicatio	Human wild-type E-Cadh	Peptide combining with	Full length human cadh	Human cadherin-13.
	1.84e+0	1.84e+0	1.84e+0	1.84e+02	1.84e+02	1.84e+02	1.47e+0	1.47e+0	1.47e+02	1.47e+02	1.18e+0	1.18e+0	1.18e+0	9.36e+0	. 366	9.36e-0	. 36	9.36e-01	. 36	7.45e+01	7.45e-01

ALIGNMENTS

88888	ឧឧឧ	8888	8888	800	P P	PR	PA	ק קיק	P P G	S E	Z Z	€ €	Z D	P A	RESULT
derived from the human desmoglein protein (amino acids 97-111) and is implicated as a self epitope in pemphigus vulgaris. Peptides derived from the human desmoglein protein are described in w04841-47. Sequence 15 AA;		colerising an individual to that polypeptide. In both cases, the polypeptide (whether self or non-self) includes an amino acid sequence corresponding to a sequence motif for a MHC class II	either an isolated human non-collagen or non-myslin basic protein (MBP) polypeptide which is capable of tolerising an individual to an autoantigen; or an isolated human pathogen polypeptide capable of	auto-immune disease Claim 1; Page 38: 58pp; English. Pharmaceutical preparations for tolerisation to antigens comprise	antigens - useful in disease treatment, and method for identification of other self and non-self antigens implicated in	WPI; 96-425218/42. Pemphigus vulgaris auto-antigens and multiple sclerosis non-self	(HARD) HARVARD COLLEGE. Strominger JL, Wucherpfennig KW;	07-MAR-1996; U03182. 07-MAR-1995; US-400796.	W09627387-A1. 12-SEP-1996.	influenza; haemagglutinin; reovirus; sigma protein.	herpes Simplex virus; adenovirus; phosphomannomutase;	autoantigen; HLA; human leukocytegen; multiple sclerosis; pemphigus vulgaris; desmociein; multiple sclerosis;	Self epitope of desmoglein 3, implicated in autoimmune disease.	; -1997 (first entry)	LT 1 W04842 standard; peptide; 15 AA.

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18-MAY-1994; 129556.

18-MAY-1994; JP-129556.

(KURS) KURARAY CO LTD.

WPI: 96-045392/05.
                                                                                                                                                                                                                                                                                        23-JUL-1996.
30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T.
WPI; 96-388562/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases related to the antibody
Claim 1: Page 2: 7pp: Japanese.
A new peptide is disclosed which contains at least 5 contiguous aming
acids from the sequence val Gly Ile Asp Gln Pro Pro Phe Gly Ile Phe
val Val Asp Lys Asn Thr Gly Asp Ile Asn Ile Thr Ala Ile Val Asp Arg
Val Use present sequence, the peptide not containing more than
50 residues. The peptide combines with anti-interepidermal cellular
antibody. It can be immobilised on a carrier to prepare an absorbent
useful for the treatment of diseases related to anti-interepidermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-1996 (first entry)

peptide combining with anti-interepidermal cellular antibody.

anti-interepidermal cellular antibody; autoantibody; adsorben

Synthetic.
                                                                                                             Fused protein recognised by pemphigus vulgaris auto:antibody - useful to treat and diagnose pemphis vulgaris (PV) antigen (Claim 1; Page 7-9; 9pp; Japanese. W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients with pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgGl hinge region and the resulting fusion protein is useful to treat or diagnose pemphigus vulgaris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-interepidermal cellular antibody-combining peptide - which be immobilised on column to form adsorbent useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cellular antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                          Pemphigus vulgaris antigen protein extracellular region. Autoantibody: immunoglobulin G; IgGl; fusion protein; diagnosis; treatment; pemphigus vulgaris; PV; bulla; blister; skin disease;
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
J08188540-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          W07908;
29-JAN-1997
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                    FGIFVVDKNTGDINI 110
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15; Conservative
                                                                      Similarity
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larity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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Pred. No. 3.51e-04;
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Pred. No. 3.51e-04;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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18-MAY-1994; 129556.

18-MAY-1994; JP-129556.

(KURS) KURARAY CO LTD.

WPI; 96-045392/05.
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27-NOV-1991;
27-NOV-1991;
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R30742;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding pemphigus vulgaris antigen diagnostic and therapeutic uses Disclosure; Fig 7; Sopp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human pemphigus vulgaris 130kD antigen.
Pemphigus vulgaris; skin disease: autoantibodies;
keratinocyte cell surface antigen; glycoprotein;
                                                                                                                                                                                                                                                                                                                        Anti-interepidermal cellular antibody-combining peptide - which can be immobilised on column to form adsorbent useful for treating diseases related to the antibody Example 1; Page 4; 7pp; Japanese.

New peptides are disclosed which contain at least 5 contiguous amino acids from the sequence Val Gy Ile Asp Gln Pro Pro Phe Gly Ile Phe acids from the sequence Val Gly Ile Asp Gln Pro Pro Phe Gly Ile Phe Glu Glu (see R93960), the peptide not containing more than 50 residues. The peptide combines with anti-interepidermal cellular antibody. It can be immobilised on a carrier to prepare an absorbent useful for the treatment of diseases related to anti-interepidermal cellular antibody. The present sequence is a specific example of the new peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R93961
R93961;
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(USSH ) US DEPT HEALTH (
Amagai M, Klaus-kovtun
WPI: 93-067436/08.
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J07309893-A.
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Sequence ]
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Local Similarity 100.0%;
hes 15; Conservative
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                                           FGIFVVDKNTGD
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999 AA;
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n V, Stanley JR;
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                                                                                                                                            Score 86; DB 1; 1
Pred. No. 4.92e-02
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Mismatches
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RESULT ID R

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                                                                                   Pemphigus foliaceus antigen-IgG constant region fusion protein - linked through the hinge region used to treat pemphigus foliaceus Claim 1; Page 10-12; 17pp; Japanese.

Claim 1; Page 10-12; 17pp; Japanese.

Claim 1; Page 10-12; 17pp; Japanese.

Chis sequence represents a fused protein recognised by pemphigus foliaceus patient autoantibody which comprises the constant region of IgG linked to the extracellular region of pemphigus foliaceus is antigen protein through the hinge portion. Pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus. The antigen is especially administered through an adsorbent upon which the fusion useful for detecting pemphigus foliaceus antibodies which is useful in immunodiagnosis. The fusion protein has little or no side effects.
   Query Match
Best Local Similarity
Matches 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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Example 2: Page 5: 7pp: Japanese.

New peptides are disclosed which contain at least 5 contiguous amino acids from the sequence Val Gly Ile Asp Iln Pro Pro Phe Gly Ile Phe Val Val Asp Lys Asn Thr Gly Asp Ile Asn Ile Thr Ala Ile Val Asp Arg Glu Glu (see R93960), the peptide not containing more than 50 residues. The peptide combines with anti-interepidermal cellular antibody. It can be immobilised on a carrier to prepare an absorbent useful for the treatment of diseases related to anti-interepidermal cellular antibody. The present sequence is a specific example of the new peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dermatitis |
Chimeric - |
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05-JUL-1995 (first entry)
Peptide combining with anti-interepidermal cellular antibody.
anti-interepidermal cellular antibody; autoantibody; adsorbent.
Synthetic.
J07309893-A.
28-NOV-1995.
18-MAY-1994; J129556.
18-MAY-1994; JP-129556.
(KURS ) KURARAY CO LTD.
MPI; 96-045392/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W15489
W15489,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pemphigus foliaceus antigen-IgG constant region fusion protein. Pemphigus foliaceus; autoantibody; constant region; IgG; extracellular region; antigen; hinge portion; skin; dermalitis herpetiformis; fusion protein; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                          J09077800-A.
25-MAR-1997.
12-SEP-1995; Z60899.
12-SEP-1995; JP-260899.
                                                                                                                                                                                                                                                                                                                                          P-PSDB; T66428.
                                                                                                                                                                                                                                                                                                                                                         (NISH/) NISHIKAWA T. WPI: 97-241758/22.
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                                                                          immunodiagnosis.
quence 778 AA;
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Similarity 100.0%;
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larity 60.0%;
Conservative
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1. .545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Pemphigus foliaceus antigen protein"
Score 84; DB 1; I
Pred. No. 8.20e-02;
5; Mismatches 1
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Pred. No. 4.92e-02;
0; Mismatches 0;
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                                   Length 778;
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ID W13009;
AC W13009;
DT 21 NOV-
DT 21 NOV-
DE Segment
KW Desmoso;
KW Carcino;
KW microme
KW microme
KW metasta
OS Homo sa;
PR 123-AUG-
PR 23-AUG-
PR (PROG-)
PA (PROG-)
PA (PROG-)
PT Surface
PT Surface
PT Autibod;
PT Claim 7
CC Carcino;
CC carcino;
CC diegeoc
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CC microme
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              RESULT AC Y. AC Y.
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Best Local S
Matches
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New isolated Helicobacter pylori nucleic acids products for the diagnosis, prevention and trea H. pylori and other Helicobacter species Claims 37, 41; Page 264-265; 339pp; English. Recombinant or substantially pure preparations are disclosed, together with the nucleic acids
                                                                                                                                                                                                                                                                                                                                              H. pylori ORF hpTe10433_36339535_f3_3 secreted protein.
Vaccine; probe; diagnostic; ORF; cell envelope protein; secreted protein; cytoplasmic protein; cellular protein Helicobacter pylori.
W0982475-A1.
11-JUN-1998.
05-DEC 1997; U22104.
14-JUL-1997; US-891928.
05-DEC 1996; US-759625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y11097
                                                                                                                                                                                                              (ASTR ) ASTRA AB.
Alm RA, Castriotta LM,
WPI; 98-333051/29.
N-PSDB; X30626.
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Sequence
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                                                                                                                                                                                                                                                                              Doig
                                                                                                                                                                                                                                                                                     PC, Kabok Z, Smith
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Pred. No. 1.36e-01;
5; Mismatches 1;
                                                                                                                                              ic acids - use
and treatment
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       of H. pylori polypeptides encoding them. In all,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PT New isolated Helicobacter pylori nucleic acids - used to develop products for the diagnosis, prevention and treatment of infection by PT H. pylori and other Helicobacter species Claims 37, 41; Page 265-266; 339pp; English.

CC Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, CC 97 ORFs are shown. The proteins are variously cell envelope proteins, CC cytoplasmic proteins, secreted proteins or other cellular proteins.

CC Vaccines containing the nucleic acids or proteins are claimed, as are CC probes containing at least 8 nucleotides from the nucleic acid CC sequences. The vaccines are useful for treating or reducing the risk of CC H. pylori infections, and the probes can be used diagnostically for CC detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
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05-DEC-1997; UZ-2104.

14-JUL-1997; US-891928.

05-DEC-1996; US-759625.

25-MAR-1997; US-823745.
H. pylori GHPO 876 protein. GHPO protein; Helicobacter peptic ulcer disease. Helicobacter pylori. WO9843478-Al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ASTR) ASTRA AB.
Alm RA, Castriotta LM, Doig PC, Kabok Z, Smith WPI; 98-333051/29.
N-PSDB; X30627.
                                                                                                                 31-MAR-1999
H. pylori GH
                                                                                                                                                                    W98278 standard;
W98278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. pylori ORF hp7e10433_36339535_f3_3 secreted protein.
Vaccine: probe; diagnostic; ORF; cell envelope protein;
                                                                                                                                                                                                                                                                                                                                                                      62
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PO 876 protein
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Pred. No. 5.92e+01;
5; Mismatches 2
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d. No. 5.92e+01;
Mismatches 2;
                                                                                gastroduodenal
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                                                                             gastritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    con in the mouse osteoblastic cell in the Mouse osteoblastic cell in Mc3r3-El and from mouse liver tissue, amplified by PCR, and then Mc3r3-El and from mouse liver tissue, amplified by PCR, and then as much common DNA as possible removed by hybridisation between the 2 libraries. Residual El-specific DNA was amplified, inserted into lambda gtl0 and screened by plaque hybridisation. A minibank of 273 E-specific clones was recovered, their inserts amplified and used to screen total RNA from both cell types. One clone specific for El was identified and sequenced. The insert from this clone was used to screen cDNA prepd. from El RNA and the longest posn. insert cloned in pGEM 112f (+) to give pKOT164. This insert was sequenced: it encoded the 796 AA mouse precursor protein (044391/R49730). The osteosarcoma to identify 2 clones encoding the 2 human precursor proteins - OSF-4-1 and OSF-4-2 (044392/R49731 and 044393/R49732).
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Matches 6; Conse
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01-APR-1998; U06371.
29-JUL-1997; US-902615.
20-APR-1997; US-833457.
24-JUN-1997; US-881227.
24-JUN-1997; US-881227.
24-JUNA-) HUMAN GENOME SCI INC.
(IMMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Al-Garawi A, Kleanthous H, Miller C, Oomen RP, Tc
Al-Garawi A, Kleanthous H, Miller C, Oomen RP, Tc
API: 98-542293/46.
                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-1994.
25-AUG-1993; 113602.
28-AUG-1992; JP-230028.
(EARH) HOECHST JAPAN LTD.
Amenn E, Kawai S, Okazaki M,
WPI: 94-076152/10.
                                                                                                                                                                                                                                                                                                           encoding them
Claim 1; Page 23-27; 34pp;
cDNA libraries were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-1994 (first entry)
Sequence encoded by human
OSF-4-2; cadherin; growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases claim 8; page 315-316; 2054pp; English.

This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 12
R49732 standard;
R49732;
                                                                   respectively).
Sequence 693
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larity 46.2%;
Conservative
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                54.3%;
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factor;
                                                                                                                                                                                                                                                                                                                              English.
Score 57; DB 1;
Pred. No. 5.92e+01
5; Mismatches
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Pred.
5; M
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osteogenesis; osteoblast; therapy;
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No. 5.92e+01
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be used for
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Length 693

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Gaps

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IFVVDKNTGDIN

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IFVIDDKSGNIH 111

T 13 R49731 standard; Protein; 795

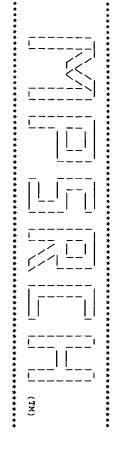
R49731;

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17-APR-1992; 872643.
19-APR-1993; US-049460.
17-APR-1992; US-872643.
01-NOV-1994; US-332638
                                                                                                                                            (DOHE-)
Suzuki S
WPI; 97-
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N-PSDB; T85403.
Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion Claim 1; Column 89-94; 56pp; English.
This sequence represents human cadherin-11. The invention specific provides details of human cadherin-5, -8, -11, -12 and -13, and rate
                                                                                                                                                                                                                                                                                                                                                                             US5646250-A.
                                                                                                                                                                                                                                                                                                                                                                                                          superfamily; cytoskeleton;
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cadherin-11.
Human; cadherin; r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New bone related, cadherin-like and diagnosis of bone metabolic
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(FARH ) HOECHST JAPAN L
Amann E, Kawai S, Oka
WPI: 94-076152/10.
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Sequence encoded by human OSF-4-1
OSF-4-1; cadherin; growth factor;
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25-AUG-1993; 113602
28-AUG-1992; JP-230
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Local Similarity 50.0%;
tes 6; Conservative
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97-362997/33.
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amily; cytoskeleton; eatenin; cancer.
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Okazaki M,
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Pred. No. 5; Misman
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d. No. 5.92e+01;
Mismatches 1;
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PT encoding them
PS Claim 1; Page 13-17; 34pp; English.
CC cDNA libraries were constructed from the mouse osteoblastic cell
CC cDNA libraries were constructed from the mouse osteoblastic cell
CC line MC3T3-El and from mouse liver tissue, amplified by PCR, and
CC then as much common DNA as possible removed by hybridisation between
CC the 2 libraries. Residual El-specific DNA was amplified. Inserted
CC into lambda gtl0 and screened by plaque hybridisation. A minibank of
CC 273 E-specific clones was recovered, their inserts amplified and
CC used to screen total RNA from both cell types. One clone specific
CC for El was identified and sequenced. The insert from this clone was
CC used to screen cDNA prepd. from El RNA and the longest posn. insert
CC cloned in pGEM 112f (+) to give pKOT164. This insert was sequenced;
CC insert was also used to screen a cDNA bank prepd. from human
CC osteosarcoma to identify 2 clones encoding the 2 human precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adhesion proteins. They are glycosylated integral membrane proteins that have an N-terminal extracellular domain that determines binding specificity, a hydrophobic membrane spanning region and a C-terminal cytoplasmic domain, which is highly conserved among members of the superfamily. The C-terminal domain interacts with the cytoskeleton through eatenins and other cytoskeleton-associated proteins. The novel cadherin proteins may be used in the analysis of the cadherin proteins in various cancers. Sequence analysis of the cadherin proteins also allows investigation of the structure and function of cadherin. The cadherin proteins may be isolated by using anti-cadherin antibodies. These antibodies may also be used to modulate the activity of cadherin and to determine the tissue specific distribution of cadherin proteins. Each subclass of cadherins has a unique tissue distribution
                                                                                                                                                                                      respectively).
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Amann E, Kawai S, Ok
WPI; 94-076152/10.
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Sequence encoded by murine OSF-4 cDNA.
Sequence encoded by murine OSF-4 cDNA.
OSF-4; cadherin; growth factor; osteogenesis; osteoblast; therapy;
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R49730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New bone related, cadherin-like OSF-4 proteins and diagnosis of bone metabolic disease, and nucl
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28-AUG-1992;
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Search completed: Sat May 13 07:05:22 2000

Job time : 7 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 07:04:49 2000; MasPar time 4.29 Seconds 164.911 Million cell updates/sec

Tabular output not generated.

Title: >US-08-991-628-2
Description: (1-15) from US08991628.pep
Perfect Score: 105

Sequence: 1 FGIFVVDKNTGDINI 15

Scoring table: PAM 150
Gap 15

Searched:

142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 26.968; Variance 38.706; scale 0.697

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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toxin, nontoxic compo	botulinum neurotoxin-	cadherin 1 precursor	probable acylamino-ac	hypothetical protein	hypothetical protein	cadherin 13 precursor	cell division protein	protein-tyrosine kina	E-cadherin precursor,	probable lipoprotein	cadherin 11 precursor	OB-cadherin precursor	cadherin-11 - mouse	cadherin-ll - mouse	tldD homolog PH0246 -	ribonuclease hii - He	ribonuclease HII - He	polyprotein - parsnip	BH-protocadherin PCDH	BH-protocadherin PCDH	מנו לייטרטרמקייקי דיו ירטיי
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ALIGNMENTS

Query Match Best Local Simi Matches 15;	SUMMARY	937-966 110,180,545	616-639 640-999	270-383 390-495 496-598	50-615 52-157 160-267	1-23 24-49 50-999	#gene ##CTOSS-TE! #map_position CLASSIFICATION KEYWORDS FEATURE	#ACCESSION A41088 #ACCESSION A41088 ##molecule_type mRNA ##residues 1-99 ##cross-references GENETICS		RESULT 1 ENTRY TITLE TITLE ALTERNATE_NAMES ORGANISM DATE DATE
100.0%; Score 105; DB 1; Length 999; Similarity 100.0%; Pred. No. 1.33e-09; 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	predicted #length 999 #molecular-weight 107502 #checksum 8311	#domain desmoglein repeat #label DG1\ #domain desmoglein repeat #label DG2\ #binding_site carbohydrate (Asn) (covalent) #status	transmembrane *status predicted intracellular *status predicted	cadherin repeat homology #label cadherin repeat homology #label cadherin repeat homology #label	<pre>#domain extracellular #status predicted #label EXT\ #domain cadherin repeat homology #label CR1\ #domain cadherin repeat homology #label CR2\</pre>	<pre>#domain signal sequence #status predicted #label SIG\ #domain propeptide #status predicted #label PRO\ #product desmoglein homolog #status predicted #label MAT\</pre>	me GDB:DSG3 ##cross-references GDB:134030; OMIM:169615 p_Dosition 18q12.1-18q12.2 FICATION #superfamily cadherin; cadherin repeat homology Calcium binding; cell adhesion; duplication; glycoprotein; DS transmembrane protein	cession A41088 resion TA41080 ##molecule_type mRNA ##rcsidues 1-999 ##label AMA ##cross-references GB:M76482; NID:g190751; PIDN:AAA60230.1; PID:g190752	A41088 RENCE A41088 authors Anagai, M.; Klaus-Kovtun, V.; Stanley, J.R. journal Cell (1991) 67:869-877 title Autoantibodies against a novel epithelial cadherin in pemphigus vulgaris, a disease of cell adhesion.	IJHUG3 *type complete desmoglein 3 precursor · human pemphigus vulgaris antigen #formal_name Homo sapiens *common_name man 30-Jun-1993 *sequence_revision 30-Jun-1993 *text_change 22-Jun-1999

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#gene
CLASSIFICATION
KEYWORDS
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#title Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type cross-references MUID:92037656
#accession A38872
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Cowin, P.

#journal Biochem. Biophys. Res. Commun. (1990) 173:1224-1230

#title Desmoglein shows extensive homology to the cadherin family of
cell adhesion molecules.

#cross-references MUID:91097553

#accession A37785
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##cross-references EMBU:X57784; NID:g436061; PIDN:CAA40930.1;
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#superfamily cadherin; cadherin repeat homology
calcium binding; cell adhesion; duplication; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koch, P.J.; Walsh, M.J.; Schmelz, M.; Goldschmidt, M.D. Zimbelmann, R.; Franke, W.W. Eur. J. Cell Biol. (1990) 53:1-12
Identification of desmoglein, a constitutive desmosomal glycoprotein, as a member of the cadherin family of constitution of desmosomal glycoprotein.
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876-905
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Poynter, D.; Arnemann, J.; Rutman, A.J.; Pidsley, S.C.;
Watt, F.M.; Ress, D.A.; Buxton, R.S.; Magee, A.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:4796-4800
Desmosomal glycoprotein DGI, a component of intercellular desmosome junctions, is related to the cadherin family cell adhesion molecules.
#cross-references MUID:91271279
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1-1049 ##label BUX
##cross-references EMBL:X56654; NID:g30505; PIDN:CAA39976.1; PID:g30506
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J. Cell Sci. (1991) 99:809-821
Structural analysis and expression cadherin-like component of the de
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desmoglein | precursor - human
desmosomal glycoprotein |
#formal_name Homo sapiens #common_name man
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Wheeler, G.N.; Buxton, R.S.; Parker, A.E.; Rees, D.A.; King, I.A.; Magee, A.I.
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##molecule_type mRNA
777-1117 ##label KOC
                                                                                                                                          #title Complete amino acid sequence of the epidermal precursor polypeptide and identification of of desmoglein gene.
#cross-references_MUID:92037656
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#accession A61
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#domain intracellular #status predicted #label INT\
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#map_position 18q12.1-18q12.2
CLASSIFICATION #superfamily cadherin; cadherin repeat homology
KEYWORDS calcium binding; cell adhesion; duplication; glycoprotein;
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Best Local Similarity 60.0%;
Matches 9; Conservative
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#title Cloning and sequence analysis of desmosomal glycoproteins and 3 (desmocollins): cadherin-like desmosomal adhesion molecules with heterogeneous cytoplasmic domains.
#cross-references MUID:91185414
#accession A38456
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#title
                                                                                                                              #authors Holton, J.L.; Kenny, T.P.; Legan, P.K.; Collins, J.E.
J.N.; Sharma, R.; Garrod, D.R.
#journal J.Cell Sci. (1990) 97:239-246
Desmosomal glycoproteins 2 and 3 (desmocollins) show
N-terminal similarity to calcium-dependent cell-cel
adhesion molecules.
#cross-references MUID:91115997
#accession A60714
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1-32;65-76;148-159;164-176;190-205;208-219;238-256;
##residues 1-32;65-76;148-159;164-176;190-205;208-219;238-256;
##experimental_source muzzle epithelium
##note sequence extractor from the sequence ext
                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type mRNA
##residues 606-761 ##label COL
##cross-references EMBL:X56967; NID:g310; PIDN:CAA40287.1; PID:g311
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##molecule_type mRNA
##residues 1-761 ##label KOC
##cross-references GB:X58029; GB:S57985; NID:g453583; PIDN:CAA41088.1:
##cross-references PID:g453584
                                                    ##molecule_type protein
##residues 1-6,'A',8-9,'R',11-17,'RCE',21-23 ##label HOL
                          ##experimental_source
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desmocollin BDCM; desmosomal glycoprotein 2
#formal_name Bos primigenius taurus #common_name cattle
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
22-Jun-1999
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Differentiation (1991) 47:29-36
Amino acid sequence of bovine muzzle epithelial derived from cloned cDNA: a novel subtype of c
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#domain cadherin repeat homology #label CR2
#length 1117 #molecular-weight 122384 #checksum
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Pred. No. 1.63e-04;
5; Mismatches 1
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J.E.; Keen,

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1-561
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Best Local S
Matches
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Best Local Similarity 61.5%;
Matches 8; Conservative
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#journal Development (1995) 121:1321-1332
#title Neural crest cell-cell adhesion controlled by sequential and
#title subpopulation-specific expression of novel cadherins.
#cross-references_MUID:95309115
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223-338
339-444
445-561
562-582
583-761
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##croses-references GB.D42155; NID:g868000; PIDN:BAA07721.1; PID:g868001
##croses-references GB.D42155; NID:g868000; PIDN:BAA07721.1; PID:g868001
##croses-references GB.D42155; NID:g868000; PIDN:BAA07721.1; PID:g868001
##croses-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-references-referen
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Similarity 53.88;
IJBODF #type complete desmocollin 1b precursor desmosomal glycoprotein 3
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cadherin-7 chicken
*formal_name Gallus gallus *common_name chicken
21-Feb-1997 *sequence_revision 21-Feb-1997 *text_change
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kinase II) #status predicted
jth 761 #molecular-weight 85170 #checksum 3508
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*binding_site phosphate (Ser) (covalent) (by casein kinase II) *status predicted\
*binding_site phosphate (Ser) (covalent) (by protein kinase C) *status predicted\
*binding_site phosphate (Tyr) (covalent) *status
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*domain intracellular *status predicted *label INT\
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#domain extracellular #status predicted #label EXT\
#domain cadherin repeat homology #label CR1\
#domain cadherin repeat homology #label CR2\
#domain cadherin repeat homology #label CR4\
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kinase C) #status predicted\
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Pred. No. 2.64e-01;
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Pred. No. 2.64e-01;
4; Mismatches 2
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#accession A39377
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#accession B38456
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#residues 1-839 ##label COL
##ress-references GB:X56966; NID:g315; PIDN:CAA40286.1;
#WCE A39377
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Similarity 53.8%;
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J. Cell Biol. (1991) 113:381-391
Cloning and sequence analysis of desmosomal glycoproteins and 3 (desmocollins): cadherin-like desmosomal adhesion molecules with heterogeneous cytoplasmic domains.
B48910 #type fragment
desmocollin lb precursor
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alternative splicing; calcium binding; cell adhesion;
duplication; glycoprotein; phosphoprotein; transmembrane
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part of this sequence, including the amino end of the mature protein, was confirmed by protein sequencing
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binding_site phosphate (Thr) (covalent) (by casein
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#domain propeptide #status predicted #label PRO\
#product desmocollin lb #status experimental #label XX
#domain extracellular #status predicted #label EXT\
#domain cadherin repeat homology #label CR1\
#domain cadherin repeat homology #label CR3\
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domain intracellular #status predicted #label INT\
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Pred. No. 2.64e-01
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human (fragment)
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#map_position 18q12.2-18q12.2
CLASSIFICATION #superfamily cadher
KEYWORDS alternative collectors
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#map_position 18q12.2-18q12.2
CLASSIFICATION #superfamily cadherin; cadherin repeat homology
KEYWORDS alternative splicing; calcium binding; cell adhesion;
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#accession A48910
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#journal Genomics (1993) 18:185-194
#title Cloning of the cDNA (DSC1) coding for human type 1
desmocollin and its assignment to chromosome 18
#cross-references MUID:94116981
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##molecule_type mRNA
##residues 1-770 ##label KIN
##cross-references GB:X72929
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##residues 1-824 ##label KIN
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FGIFVVDKNTGDI 13
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desmocollin la precursor - human (fragment)

#formal_name Homo sapiens #common_name man

08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change

15-Aug-1997
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alternative splicing; calcium binding; cell adhesion;
glycoprotein; phosphoprotein; transmembrane protein
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Cloning of the cDNA (DSC1) coding for human type 1 desmocollin and its assignment to chromosome 18.
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Pred. No. 4.08e-01;
"""matches 2;
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Pred. No. 4.08e-01
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##molecule_type mRNA
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##cross-references EMBL: 734522; N.
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FICATION #superfamily cadherin repeat homology
#length 840 #molecular-weight 93848 #checksum 31
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##residues 1-840 ##label RES
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Similarity 53.8%;
7; Conservative
                  $59969 *type complete
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) isoform
beta - (Chinese hamster
DNA topoisomerase II isoform beta; DNA-gyrase
#formal_name Cricetulus griseus #common_name Chinese hamst
15-Feb-1996 #sequence_revision 13-Mar-1997 #text_change
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#formal_name Homo saptens #common_name man
12-Aug-1996 #sequence_revision 12-Aug-1996
20-Aug-1999
                                                                                                                                                                                                                                                                                                      #superfamily cadherin; cadherin repeat
#length 894 #molecular-weight 100044
                                                                                                                                                                                                                                                                                                                                                                                                                                                      I37282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theis, D.G.; Koch, P.J.; Franke, W.W. Int. J. Dev. Biol. (1993) 37:101-110 Differential synthesis of type 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #formal_name Homo sapiens *common_name man
12-Aug-1996 *sequence_revision 12-Aug-1996 *text_change
20-Aug-1999
                                                                                                                                                                                                                                                                                                                                        829/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor
                1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *type complete
                                                                                                                                                                                                                                      Score 65; DB 2;
Pred. No. 4.08e-01
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65; DB 2;
Pred. No. 4.08e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    NID: g505536; PIDN: CAA84279.1;
                                                                                                                                                                                                                                                                      Length 894;
                                                                                                                                                                                                                                                                                                                                                                                                                                   GB/EMBL/DDBJ
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*checksum
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                                        Chinese hamster
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FEATURE
697-927
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ENTRY
TITLE
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CLASSIFICATION #superfamily eukaryotic type II DNA topoisomerase; phage
DNA topoisomerase (ATP-hydrolyzing) medium chain homolo
KEYWORDS ATP; DNA binding; DNA replication; isomerase; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATE_NAMES
CONTAINS
ORGANISM
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Cloning and characterization of full-length cDNAs coding for the DNA topoisomerase II beta from Chinese hamster lung
#cross-references MUID:96085121
#scression S59969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
Matches 8: Conser
                                                                                                                                                                                                                                                                                               #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal
                                   #authors Chung, T.D.Y.; Drake, F.H.; Tan, K.B.; Per, S.R.; Crooke, S.T.; Mirabelli, C.K.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:9431-9435
#title Characterization and immunological identification of cDNA
#title clones encoding two human DNA topoisomerase II isozymes
#cross-references MUID:90083281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome 3p24.
*cross-references MUID:93087165
                                                                                                                                                                                                                                      *accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                              *accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *authors
                                 #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          922 IFVVDRNTVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type mRNA
##residues 1-1612 ##label DER
                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
#residues 1-23,29-1626 ##label JEN
##cross-references EMBL:X68060; NID:g37230; PIDN:CAA48197.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##cross-references EMBL: x86455; NID: g790987; PIDN: CAA60173.1;
                ##molecule_type
                                                                                                                                                       **cross-references GB:M27504
                                                                                                                                                                                                                 **molecule_type mRNA
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DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) beta,
splice form 2 - human
DNA topoisomerase II isoform beta-2
DNA topoisomerase II isoform beta-2
DNA topoisomerase II isoform beta-1
*formal_name Homo.sapiens *common_name man
04-Oct.1991 *sequence_revision 03-May-1996 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jenkins, J.R.; Ayton, P.; Jones, T.; Davies, S.L.; Simmons, D.L.; Harris, A.L.; Sheer, D.; Hickson, I.D. Nucleic Acids Res. (1992) 20:5587-5592 Isolation of cDNA clones encoding the beta isozyme of human DNA topoisomerase II and localisation of the gene to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #domain phage T4 DNA topoisomerase (ATP-hydrolyzing)
medium chain homology #label T4T
#length 1612 #molecular-weight 182074 #checksum 5332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S26730; A39242; S10710; S33970; S30191; S41641; S30190 S26730
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mRNA
1043-1276 ##label
                                                                                                                                                                                                149-1043 ##label CHU
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72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 61; DB 2; I
Pred. No. 2.22e+00;
2; Mismatches 1
AUS
                                                                       of a human cDNA clone enco
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KEYWORDS
FEATURE
1-1626
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#map_position 3p24-3p24
CLASSIFICATION #superfamily eukaryotic type II
                                                                                  ACCESSIONS
REFERENCE
                                                                                                                                        ORGANISM
DATE
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ENTRY
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARY
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Best Local
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#journal
#title
                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #cross-references MUID:9
#accession $33970
##molecule_type mRNA
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                                                                 #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##cross references EMBL:X71911
##note this possite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type mRNA 596-1430,'S',1432-1610,'A',1612-1626 ##label AU1 ##cross-references EMBL:Z15115; NID:9288564; PIDN:CAA78821.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-23,29-1610,'A',1612-1626 ##label ##cross-references EMBL:Z15111
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                                                                                                                                                                                                                                                                                                                           934 IFVVDRNTVEI 944
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                                                                                                                                                                                                                                                                                                                                                           h 58.1%;
Similarity 72.7%;
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Austin, C.A.; Sng, J.H.; Patel, S.; Fisher, L.M. Biophim. Biophim. Biophimerase II is the II-beta isoform: coding sequence and homology with other type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #superfamily eukaryotic type II DNA topoisomerase: phage T4
DNA topoisomerase (ATP-hydrolyzing) medium chain homology
alternative splicing; ATP; dimer; isomerase; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S41641
         Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shav
                                                                                                                     A65141 *type complete hypothetical 10.6 kD protein in capacity formal_name Escherichia coli 12-Sep-1997 *sequence_revision 1: 14-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                     #length 1626
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Kirkpatrick, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                  #product DNA topolsomerate (ATP-hydrolyzing)
#label MAJR\
#domain phage T4 DNA topolsomerase (ATP-hydrolyzing)
medium chain homology #label T4T
medium chain homology #label T4T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:x53662; GB:S56813; NID:g38324; PIDN:CAA37706.1; PID:g38325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA topoisomerase II beta-1 #status predicted
                                                                                                                                                                                                                                                                                                                                                             Score 61; DB 2; I
Pred. No. 2.22e+00;
2; Mismatches 1
                                                                                                                                          17-Sep-1997
                                                                                                                                                                                            gntR-ggt intergenic
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September 1992
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#journal

Science

(1997)

277:1453-1462

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**CCESSIONS $76379

**REFERENCE $74322

**Bauthors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;

**Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.;

**Sasamoto, S.; Kimura, T.; Hosouchi, T.; Mateuno, A.;

**Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo,

**S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;

**Yasuda, M.; Tabata, S.

**Journal DNA Res. (1996) 3:109-136

**Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

**Cross-references MUID:97061201

**accession $76379

**preliminary
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SUMMARY
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REFERENCE
#authors
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DATE
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ENTRY
TITLE
Search completed: Sat May 13 07:04:57 2000 Job time : 8 secs.
                                                                                                                                                                                                                                                                     SUMMARY
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                                                                                                                                                                             Query Match 57.1%;
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.1%;
Best Local Similarity 45.5%;
Matches 5; Conservative
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#cross-references MUID:97426617
#accession A65141
                                                                                                                                                                                                                                                                                                                                 ##status preliminary
##molecule_type DNA
1-214 ##label KAN
##residues 1-214 ##label KAN
##cross-references EMBL.D64000; GB:AB001339; NID:g1001484; PID:d1010882;
##cross-references EMBL.D64000; GB:AB001339; NID:g1001484; PID:d1010882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type DNA
##residues 1-94 ##label BLAT
##cosg-references GB:AE000421; GB:U00096; NID:g1789854; PID:g1789855;
##crperimental_source strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                               ##note
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                                                                                                               49 FGVLMIDPSTGEIS 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 FVVDKNTGDIN 14
                                                                                          FGIFVVDKNTGDIN 14
                                                                                                                                                                                                                                                              the nucleotide sequence was submitted to the EMBL Data
Library, June 1996
#length 214 #molecular-weight 24539 #checksum 4859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yrhB
#length 94 #molecular-weight 10613 #checksum 4152
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                                                                                                                                                                                                  Score 60; DB 2; Length 214; Pred. No. 3.36e+00;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Sat May 13 06:58:15 2000: MasPar time 99.86 Seconds 4.575 Million cell updates/sec

Description: Perfect Score: Sequence: Title: >US-08-991-628-2 (1-15) from US08991628.pep 105 1 FGIFVVDKNTGDINI 15

Tabular output not generated.

Scoring table:

PAM 150 Gap 15

Post-processing:

83857 segs, 30454973 residues

Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 27.553; Variance 34.618; scale 0.796

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222118	Result
105 888 884 887 888 888 888 888 888 888 888	Score
100.0 80.0 78.1 78.1 58.1 58.1 58.1 57.1 57.1 57.1 57.1 57.1 57.1 57.1 57	Query Match
1043 11043 11043 11043 11043 11043 893 894 1612 1612 1627 94 1627 794 209 209 209 209 209 209 209 209 209 209	Length I
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2.32e-11 4.29e-06 4.29e-05 5.19e-05 5.62e-01 5.6	Pred. No.

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ENDOTHELIAL ACTIN-BIND	BRAIN-CADHERIN PRECURS	HYPOTHETICAL PROTEIN M	DNA-DIRECTED RNA POLYM	DNA-DIRECTED RNA POLYM	HYPOTHETICAL 38.5 KD P	28 KD OUTER MEMBRANE P	HYPOTHETICAL 19.5 KD P	SUCRASE-ISOMALTASE, IN	SUCRASE-ISOMALTASE, IN	PUTATIVE RNA-DIRECTED	BOTULINUM NEUROTOXIN T	AMINOPEPTIDASE N (EC 3		EPITHELIAL-CADHERIN PR	PLACENTAL-CADHERIN PRE	CADHERIN-6 PRECURSOR (CADHERIN-6 PRECURSOR (B-CADHERIN PRECURSOR (HYPOTHETICAL 62.8 KD T	CADHERIN-10 PRECURSOR.	DITCIDELICATION OF . AC A
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01-OCT-1993;
01-OCT-1993;
01-NOV-1997
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SEQUENCE
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Koch P.J.,
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"Identification of desmoglein, a constitutive desmosomal glycoprotein, as a member of the cadherin family of cell molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
Goodwin L., Hill J.E., Raynor K., Raszi L., Manabe in Desmojein shows extensive homology to the cadheri adhesion molecules.";
Biochem. Biophys. Res. Commun. 173:1224-1230(1990).
-:- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME.
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS.
FILAMENTS MEDIATING CELL-CELL ADHESION.
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REPEAT
                                                                                                                                                "Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene. Eur. J. Cell Biol. 55:200-208(1991).
                                                                                                                                                                                                                        REVISIONS, AND SEQUENCE OF MEDLINE; 92037656.
                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-MUZZLE EPITHELIUM;
Koch P.J., Goldschmidt M.D.,
Submitted (MAR-1991) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota: Metazoa: Chordata: Craniata;
Eutheria: Cetartiodactyla: Ruminantia; i
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15; Conser
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91097553.
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(Rel. 27, Last sequence update)
(Rel. 35, Last annotation update)
1 PRECURSOR (DESMOSOMAL GLYCOPROTEIN I) (DG1).
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larity 100.0%;
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EMBL/GenBank/DDBJ databases.
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DESMOGLEIN 3.
EXTRACELLULAR (POTENTIAL).
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No. 2.32e-11;
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TISSUE-KERATINOCYTES:

MEDLINE: 91271279.

Wheeler G.N., Parker A.E.,

Arnemann J., Rutman A.J., F

Buxton R.S., Magee A.I.;

"Desmosomal glycoprotein DC
                                                                                                                                                                           DSG1_HUMAN STANDARD;
Q02413;
Q1-207-1993 (Rel. 27, Cr
Q1-0CT-1993 (Rel. 27, La
Q1-NOV-1997 (Rel. 35, La
DESMOGLEIN 1 PRECURSOR (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X58466; CAA41380.1; -.
EMBL; X57784; CAA40930.1; -.
EMBL; M58165; AAA62709.1; -.
EMBL; S14603; IJBOC1.
                                                                                                                   Homo sapiens (Human).
Homo sapiens (Human).
Craniata; Vertebrata;
Craniata; Vertebrata;
Craniata; Vertebrata;
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Cell adhesion; Signal; Transmembrane;
Calcium-binding; Repeat.
                                                                                        EQUENCE FROM N.
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TISSUE SPECIFICITY: EPIDERMIS, MUZZLE, TONGUE AND
DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
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SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY
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PS00232; CADHERIN;
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                                          Parker A.E.,
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R (DESMOSOMAL GLYCOPROTEIN 1)
DGI,
                             , Thomas
Pidsley
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Pred. No. 4.29e-06;
5; Mismatches 1
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CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
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POTENTIAL.

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M; ADE46133F8B77C11 CRC64;
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                             Ataliotis P., Watt F.M., Ree
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REPEATS
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PIR; S16906; IJHUG1.
HSSP; P09803; IEDH.
MIM; 125670; -.
PROSITE; PS00232; CADHERIN; 2
PRAM; PF00028; cadherin; 4
Cell adhesion; Signal; Transm
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Q14126;
Q1-NOV-1997
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                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-: FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.

-: INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEL FILAMENTS MEDIATING CELL-CELL ADHESION.

-: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-: TISSUE SPECIFICITY: EPIDEMNIS, TONGUE, TONSILAND ESOPHAGUS.

-: DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                       01-NOV-1997 (Rel. 35, C
01-NOV-1997 (Rel. 35, I
01-NOV-1997 (Rel. 35, I
DESMOGLEIN 2 PRECURSOR
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SIMILARITY: BELONGS
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Similarity 60.0%;
9; Conservative
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R (HDGC).
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CADHERIN 4.
DESMOGLEIN REPEAT 1.
DESMOGLEIN REPEAT 3.
DESMOGLEIN REPEAT 4.
DESMOGLEIN REPEAT 5.
GLY/SER-RICH.
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DESMOGLEIN 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASNIC (POTENTIAL).
CADHERIN 2.
CADHERIN 2.
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Pred. No. 4.29e-06;
5; Mismatches 1
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AND INTERMEDIATE
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HSSP; P15116; INCI.
MIM; 125671; -.
PRINTS; PR00205; CADHERIN.
PROSTE; PS00232; CADHERIN; 3.
PROM; PF00028; Cadherin; 4.
PRAM; PF00028; Cadherin; 4.
                                                                                                                                                                                                                      REPEAT
RE
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DOMAIN
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"Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene."

EUR. J. Cell Biol. 55:200-208(1991).

-!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.

INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

-!- TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND CARCINOMAS.

-!- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoskeleton;
SIGNAL
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-i- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY
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FGIFVVDKNTGDINI
                                                    FGIFVFNKDTGELNV
                                                                                                           Similarity
9; Conser
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                                                                                                     Score 82; DB 1;
Pred. No. 1.28e-05
5; Mismatches
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POTENTIAL.
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DESMOGLEIN 2.
EXTRACELLULAR (
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CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
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CADHERIN
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                                                                                                                                                                                                                223B897FED70B289 CRC64;
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REPEAT
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REPEAT
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01-FEB-1994
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DESMOCOLLIN
DSC1
This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                 Holton J.L., Kenny T.P., Legan P.K., Collins J.E., Keen J.N., Sharma R., Garrod D.R.; "Desmosomal glycoproteins 2 and 3 (desmocollins) show N-terminal similarity to calcium-dependent cell-cell adhesion molecules."; J. Cell Sci. 97:239-246(1990).
                                                                                                                                                                                                                                                                                 "Size heterogeneity, phosphorylation and transmembrane organisation of desmosomal glycoproteins 2 and 3 (desmocollins) in MDCK cells."; J. Cell Sci. 96:339-248(1990)
-i- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOL
                                                                                                                                                                                                                                                                                                                                             MEDLINE; 91009551.
Parrish E.P., Marston
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 133-155.
MEDLINE: 91115997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (1B), AND P MEDLINE; 91239591.
Mechanic S., Raymor K., Hill J "Desmocollins form a distinct adhesion molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garrod D.R.; Cloning and sequence analysis of desmosomal glycoproteins 2 and (desmocollins): cadherin-like desmosomal adhesion molecules with heterogeneous cytoplasmic domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-EPIDERMIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovinae; Bos [1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collins J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE: 91185414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Amino acid sequence of bovine muzzle epithelial desmocollin derived from cloned cDNA: a novel subtype of desmosomal cadherins.";
                                                                                                                                             desmosomal glycoproteins 2 and 3 (desmocollins) in MDCK cells.";

Cell Sci. 96:239-248(1990).

FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS. LINKED TO THE KERATINIZATION OF EPITHELIAL TISSUES.

TO THE KERATINIZATION OF EPITHELIAL TISSUES.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: TWO FORMS; LADG2 (SHOWN HERE) AND 1B/DG3; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EPIDERMIS AND WEAKLY IN TONGUE PAPILLAE.

DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
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SIMILARITY: BELO
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aryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
heria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                      (POTENTIAL)
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Biol. 113:381-391(1991).
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(Rel.
1A/1B
                                                                                                BELONGS TO THE CACHERIN FAMILY. DESMOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A: a novel subtype
47:29-36(1991).
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39, Last a
PRECURSOR
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R (DESMOSOMAL GLYCOPROTEIN
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                                                       restrictions
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                                  for
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Matches
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Best Local
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EMBL; X55966; CAA40287.1;
EMBL; X56967; CAA40289.1;
EMBL; X56968; CAA40289.1;
EMBL; X56968; CAA40088.1;
EMBL; X56968; CAA40088.1;
EMBL; X58029; CAA41088.1;
FIR; B38456; IJBODE
PIR; B394383; IJBODE
PIR; A39377; A39377;
HSSP; P09803; 1EDH
                                                                                                                                                                                01-NOV-1997
01-NOV-1997
15-FEB-2000
DESMOCOLLIN
                                                                                                                                  DSC1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Eukaryota; Primates; Catarrhini; Hominidae;
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CONFLICT
SEQUENCE
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REPEAT
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VARIANT
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VARSPLIC
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REPEAT
REPEAT
                                                                    Theis D.G., Koch P.J., F
"Differential synthesis
human stratified epithel
int. J. Dev. Biol. 37:10
                                  SEQUENCE FROM N.A. TISSUE-FORESKIN; Zimbelmann R.;
                                                                                                        SEQUENCE FROM N.A.
TISSUE-FORESKIN;
MEDLINE; 93283249.
                                                                                                                                                                                                                     DSC1_HUMAN
Q08554;
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SEQUENCE FROM N.A
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1A/1B
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                                                                                                                                                                                                                               STANDARD
                                                                    epithelia.";
l. 37:101-110(1993)
                                                                                                                                                                           35, Created)
35, Last sequence update)
39, Last annotation update)
PRECURSOR (DESMOSOMAL GLYCOPROTEIN 2/3) (DG2/DG3).
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485
99647
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53.8%;
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                                                                                       type
                       EMBL/GenBank/DDBJ
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Pred. No. 5.19e-02;
4; Mismatches 2;
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CADHERIN 4.
CADHERIN 5.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESMOCOLLIN 12
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                               PRT;
                                                                                       and
                                                                                                                                                                                                                               894
                                                                                      type
                                                                                                                                                   Vertebrata;
                                                                                                                                                                                                                                                                                                                                                 ISOFORM 1B).
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AR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                            ESIRGHTLVKN
                                                                                      desmocollin
                                                                                                                                                                                                                                                                                                                       Length 893;
                                                                                                                                                                                                                                                                                                                                         AND 3).
9 CRC64;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                            (ix
                                                                                      mRNAS
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                                                                                                                                                                                                                                                                                                                                                                             ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal;
                                                                                      'n
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MEDLINE; 94116981.

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Best Local S
Matches
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EMBL: 234522; CAA84278.1; -.
EMBL: 72925; CAAS1428.1; -.
EMBL: X72925; CAAS1429.1; -.
HSSP: P09803; LEDH.
MIN: 125643; -.
PRINTS: PRO0205; CADHERIN.
                                                                                                          VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                           CARBOHYD
CARBOHYD
                                                                                                                                                                                                                   REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00028; cadherin; 5.
Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     related to the desmosomal cadherins DGII/III."; FEBS Lett. 286:9-12(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 135-151 AND 283-292.
MEDLLNE: 91323543.
King I.A., Magee A.I., Rees D.A., Buxto
"Keratinization is associated with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            King I.A., Arnemann J., Spurr N.K., Buxton R.S.; "Cloning of the cDNA (DSC1) coding for human type 1 desmocollin and its assignment to chromosome 18.";
                                                                                                                                                                                                                                                                                                                                         Cytoskeleton;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00232; CADHERIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             its assignment to chromosome Genomics 18:185-194(1993).
                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                            PROPEP
                          182 FNLFYIEKDTGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO BEIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS. LINKED TO THE KERATINIZATION OF EPITHELIAL TISSUES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALTERNATIVE PRODUCTS: TWO FORMS; 1A/DG2 (SHOWN HERE) AND 1B/DG3; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: STRONGLY EXPRESSED IN EPIDERMIS, LESS IN LYMPH NODE AND TONGUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY
 FGIFVVDKNTGDI 13
                                                    h 61.9%;
Similarity 53.8%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an
                                                                                                      841
132
894
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                                                                                                                                                                                                                                                                                                                                                       Calcium
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                                                                                                                                                             354
471
575
682
165
546
840
                                                                                                           100044
                                                                                                                                                                                                                                                                                                                                                       -binding;
                                                     Pred.
                                                                                                                                                          CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
POTENTIAL.
POTENTIAL.
KVYLCGQDEEH
                                                                    Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                             ω
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                                                                                                       MISSING (IN ISOFORM 1B).
T -> S (IN REF. 3).
A; 44BA33038699E3E1 CRC64;
                                                                                                                                                                                                                                                                   POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                   1B)
                                                                                                                                                                                                                                                         CADHERIN 1.
                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                 DESMOCOLLIN 1A/1B
                                                                                                                                                                                                                                                                                                                                                    Alternative splicing
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buxton R.S.;
                                                   8.44e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                DB 1;
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                                                                                                                                                             ESIRGHTLIKN (IN ISOFORM
                                                                              Length 894;
                                                     Indels
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Best Local :
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P55849;
01-NOV-1997
01-NOV-1997
15-JUL-1998
                                                             VARSPLIC
SEQUENCE
                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  development.";

J. Invest. Dermatol. 107:531-538(1996).

J. Invest. Dermatol. 107:531-538(1996).

II FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS: INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL. ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENT ISOFORMS. LINKED TO THE KERATINIZATION OF EPITHELIAL TISSUES.

TO THE KERATINIZATION OF EPITHELIAL TISSUES.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.

PROMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:109173; DSC1.
PRINTS; PR00205; CADHERIN.
PROSITE; PS00232; CADHERIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X97986; CAA66628.1; -. EMBL; X97986; CAA66629.1; -. HSSP; P09803; IEDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   King I.A., O'Brien T.J., Buxton R.S.; "Expression of the 'skin-type' desmosomal cadherin linked to the keratinization of epithelial tissues
                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
-I- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                          REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
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                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                             840
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135
692
715
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613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 35, Created)
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                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                cadherin: 5.
Signal; Transmembrane; Cytoskeleton; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-SKIN;
                                                           886
98953
                                                                                                                        58.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative splicing
                                                               ž
Score
Pred.
                                                                                                                                                                                                                   CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
                                                                                                                    POTENTIAL.
POTENTIAL.
KVYLCGQAEEH
                                                           MISSING (IN ISOFORM 1B)
F34F8D8578CE92F7 CRC6
                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
DESMOCOLLIN 1A/1B.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                POTENTIAL
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N 61;
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DB 1; L
5.62e-01;
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                                                                                                                      ESIRGHTLIKN
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                             TP2B_CRILO STAN

Q64399;

15-JUL-1998 (Rel. 1

15-FEB-2000 (Rel. 1

DNA TOPOISOMERASE 1
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Q64511:
15-JUL-1998 (Rel. 36, 0
15-JUL-1998 (Rel. 36, 1
15-FEB-2000 (Rel. 39, 1
DNA TOPOISOMERASE II, 1
         DNA TO
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ACT_SITE
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PRINTS; PRO0418; TPI2FAMILY.
PRINTS; PRO158; CCAATSUBUNTA.
PRINTS; PRO1158; TOPISMRASEII.
PRINTS; PRO1158; TOPISMRASEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutharia; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                       922 IFVVDRNTVEI 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTI
RELAX ONLY NEGATIVE SUPERCOILS.
SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ATP-DEPENDENT B OF DOUBLE-STRANDED DNA. SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 YNLFYIEKDTGDI
: :| ::|:|||
1 FGIFVVDKNTGDI
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; P06786; 1BGW.
MGI:98791; TOP2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TE; PS00177; TOPOISOMERASE_II; 1. PF00204; DNA_topoisoII; 1.
                                                                                                                                                                                                                                                                                                                                      Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOISOII; 1.
Topoisomerase; DNA-binding; ATP-binding; Nuclear 170 175 ATP (POTENTIAL).

814 814 DNA CLEAVAGE (BY SIMILARITY).
1612 AA; 181863 MW; 331B9300651308C4 CRC64;
                                                                                                                                                                                                                                                                                                                                   58.1%;
larity 72.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                 STANDARD;
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                           36. Created)
36. Last sequence update)
39. Last annotation update)
II, BETA ISOZYME (EC 5.99.1.3).
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annotation update)
ISOZYME (EC 5.99.1.3).
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Pred. No. 5.
2; Mismatc
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                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
CLEAVAGE (BY SIM)
331B930065130BC4
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551308C4 CRC64;
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tent is in
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Best Local
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                                                                                                                                                                                                                                                                                                 002880;
01-JUL-1993 (Rel. 2
01-OCT-1993 (Rel. 2
15-FEB-2000 (Rel. 3
DNA TOPOISOMERASE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isomerase;
NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                               TOP2B.
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                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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SEQUENCE FROM N.A.

MEDLINE; 93087165.

Jenkins J.R., Ayton P., Jones T., Davies S.

Jenkins J.R., Sheer D., Hickson I.D.;

"Isolation of cDNA clones encoding the beta
topolsomerase II and localisation of the ge
Nucleic Acids Res. 20:5587-5592(1992).

[2]
                                                                                                                                                                    HOWO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve:
Eukaryota; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS: PRO0418; TPI2FAMILY.
PRINTS: PR00615; CCAATSUBUNTA.
PRINTS: PR01158; TOPISMRASEII.
PROSITE; PS00177; TOPOISOMERASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00204; DNA_topoisoII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
-!- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RELAX ONLY NEGATIVE SUPERCOILS.
SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204; DNA_topoisoII; 1.
Topoisomerase; DNA-binding; ATP-binding; Nuclee 170
ATP (POTENTIAL).
814
814
B14
DNA CLEAVAGE (BY SIMILARITY).
1612 AA; 182074 MW; CO1D6FC40620FC68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.1%;
larity 72.7%;
Conservative
                                                                                                                                                                                                                                                                           26, Created)
27, Last sequence update)
39, Last annotation updat.
II, BETA ISOZYME (EC 5.99)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61; DB 1; L
Pred. No. 5.62e-01;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                         1626
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                                        beta isozyme of human
he gene to chromosome
                                                                                                                                                                                                                                                                             5.99.1.3).
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                                                                                                                                                                                                              Vertebrata;
                                                                                                     S.L.,
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ENZYMES
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SOTITION OF THE REAL PROPERTY OF THE PROPERTY 
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Best Local S
Matches
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EMBL; X71911; -; NOT_ANNOTATED_CDS.
EMBL; Z15111; CAA78815.1; -.
EMBL; Z15115; CAA78821.1; -.
EMBL; X53662; CAA37706.1; -.
PIR; $26730; $26730.
PIR; $26730; $26730.
PIR; $41641; $41641.
HSSP; P06786; 1BGW.
                                                                                                                                                                                                                      NP_BIND
                                                                                                                                                                                                                                                                                                    PRINTS: PRO0418; TPI2FAMILY.
PRINTS: PRO0615; CCAATSUBUNTA.
PRINTS: PRO1158; TOPISMRASEII.
PROSITE: PS00177; TOPOISOMERASE_II:
PFAM: PF00204; DNA_topoisoII; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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MIM; 126431
                                                                                                                                                                                                                                                          Alternative
                                                                                                                                                                                                                                                                                 Isomerase; Topoisomerase; DNA-binding; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE SPLICING. MEDLINE: 93376494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolation and characterization of a "Isolation and characterization of a novel DNA topoisomerase II homologue FEBS Lett. 266:115-117(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Austin C.A., Sng J.H., Patel S., Fisher L.M.; "Novel HeLa topoisomerase II is the II beta isoform: con sequence and homology with other type II topoisomerases biochim. Biophys. Acta 1172:283-291(1993).
                       934
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SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: PHOSPHORYLATED.
MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: NUCLEAR; NUALTERNATIVE PRODUCTS: TWO FORMS, PRODUCED BY ALTERNATIVE SPLICING FORM IS SHOWN HERE.
IFVVDRNTVEI
                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90306333
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24
1611
1626
                                                                                                                                                                 splicing; Nuclear protein.

182 187 ATP (POTENTIAL).

1826 26 DNA CLEAVAGE (BY SIMILARITY).

28 MISSING (IN ISOFORM BETA-1).

1611 1611 T -> A (IN REF. 2).
                                                                  Conservative
                                                                                                                                     2
1611
5 AA;
                                                                                  58.1%;
                                                                                                                                                     183296 MW;
                                                           Score 61;
Pred. No.
2; Misma
                                                                                                                                                > A (IN REF. 2).
E7BE9262CC68B04D
                                                                                     No. 5.62e-01
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S, CALLED BETA-1
NG OF THE TOP2B (
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from H
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                                                                                                       DB 1;
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                                                                                                       Length 1626;
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THE BETA-2
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P46857;
01-NOV-1995 (
01-NOV-1995 (
01-NOV-1997 (
HYPOTHETICAL
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nimi A., Harata M., Mizuno S.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
MAKES DOUBLE-STRAND BREAKS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
OF DOUBLE-STRANDED DNA.
-!- SUBCELLULAR LOCATION: NUCLEAR; GENERALLY LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998
15-JUL-1998
15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TP2B_CHICK 042131;
Escherichia
                                                                                                                                                                                                                                                                                                                                               HSSP: P06786; 1BGW.
PRINTS; PR00418; TPIZFANILY.
PRINTS; PR00615; CCAATSUBUNTA.
PRINTS; PR01158; TOPISWRASEII.
PROSITE; PS00177; TOPOISOMERASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Noormathae: Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB007446; BAA22540.1; HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELAX ONLY NEGATIVE SUPERCOILS.
-!- SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS
                                                                                                                                                                                                                                                                                                                                         PFAM; PF00204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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(Rel. 39, Last annotation)
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DIA: 1.

ATP-binding: ATP-binding: Nuclear

ATP (POTENTIAL).

DNA CLEAVAGE (BY SIMILARITY).
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POLY-LYS.
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                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extra the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                   Shibata T., Shimoyama Y., Gotoh M., Hirohashi S.;

"Identification of human cadherin-14, a novel neurally specific type
II cadherin, by protein interaction cloning.";
J. Biol. Chem. 272:5236-5240(1997),
-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETEROCENEOUS CELL TYPES.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998
15-JUL-1998
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE: 97426617.
               EMBL: U59325; AAB02933.1; HSSP; P15116; 1NCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 9
                                                                                                                                                                                                                                                                                                                           MEDLINE;
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f., Shimoyama Y.,
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PIR; J01917; J01917
PFAM; PF00680; RNA_dep_RNA_pol; 1.
PFAM; PF009910; RNA_helicase; 1.
Polyprotein; ATP-binding; Coat pro
RNA-directed RNA polymerase.
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                                                                                                                                                                                                                                                                                                                                                                                                            Turnbull-Ross A.D., Reavy B., Mayo M.A., Murant A.F.;
"The nuclectide sequence of parsnip yellow fleck virus:
picorna-like virus.";
J. Gen. Virol. 73:3203-3211(1992).
-!- SIMILARITY: SOME, TO THE CMPV AND TBRV POLYPROTEINS.
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                                 Length 3027;
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2.7.7.48)].
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Indels

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2246 FGVFGVNDTIGIIDV

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Best Local s
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLLNE: 99120557.

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Carmel G.,

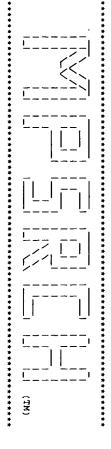
Smith D.R., Noonan B., Guild B.C., Dejonge B.L., Carmel G.,

Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,

Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UT 15
RNH2_HELDJ STANDARD: PRT: 209 AA.

Q9ZJR1:
15-FEB-2000 (Rel. 39, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
RIBONUCLEASE HII (EC 3.1.26.4) (RNASE HII).

RNHB OR HP1323.
                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Nuclease; Endonucle SEQUENCE 209 AA; 23078 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 39:176-180(1999).
-I- FUNCTION: DEGRADES THE RIBONUCLEOTIDE MOIETY ON RNA-DNA HYBRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001548; AAD06828.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter.
                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                            Local Similarity 46.28;
                                                                                                                                       Ŋ
                                                                                                                                       GIFVVDKNTGDIN
                                                                                                                                                                                                  GFFVVKKSANEID 79
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Endonuclease; Manganese.
23078 mW; F06CDEEA4C163D1D CRC64;
                                                                                                                                                                                                                                                                        Score 57; DB 1; I
Pred. No. 3.44e+00;
5; Mismatches 2
                                                                                                                                                                                                                                                                                                                                          Length 209;
                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                               Indels
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 07:00:24 2000; MasPar time 232.53 Seconds 4.473 Million cell updates/sec

Tabular output not generated.

Title:

Scoring table: Description: Perfect Score: Sequence: >US-08-991-628-2 (1-15) from US08991628.pep FGIFVVDKNTGDINI 15

PAM 150 Gap 15

Searched: 225878 segs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb112
1:sp_archea 2:sp_bacter1a 3:sp_fung1 4:sp_human
1:sp_archea 2:sp_bacter1a 7:sp_mhc 8:sp_organelle
5:sp_inage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 26.732; Variance 34.969; scale 0.764

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

21111111111111111111111111111111111111	Result
######################################	Score
55.22 55.22 55.22 55.22 55.22 55.22 55.22	Query Match
993 1329 3503 3503 214 598 593 624 1033 1033 1033 1033 1035 1069 1069 1069 11069	Length
11 13 13 13 11 10 11 10 11 10 11 11 11 11 11 11 11	BB
03590 09590 096356 024292 0258735 088735 0988735 0988733 0988733 0985914 0985914 0935914 0935945 0935945 0935945	ID
DESMOGLEIN 3 (FRAGMENT CHICKEN CADHERNN-7. C45G7.6 PROTEIN. ADHERIN. ADHERIN. HYPOTHETICAL 24.5 KD PROBABLE TUNGSTEN-CONT HYPOTHETICAL PROTEIN MYPOTHETICAL PROTEIN MYPOTHETICAL PROTEIN MYPOTHETICAL PROTEIN. CONSERVED HYPOTHETICAL LACCASE (EC 1.10.3.2). HYPOTHETICAL 68.6 KD PKIAA0345-LIKE 9. PROTOCADHERIN ALPHA 5. PARAXIAL PROTOCADHERIN NF-PROTOCADHERIN NF-PROTOCADHERIN PCDH7 (BH-PCDH)A. PCDH7 (BH-PCDH)A. PCDH7 (BH-PCDH)B.	Description
4.79e-07 5.11e-01 1.28e+00 2.02e+00 2.02e+00 3.17e+00 3.17e+00 3.17e+00 4.94e+00	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	1.2
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52.4	52.4	52.4	52.4	•	52.4	52.4	٠	•	•		53.3	•	•	•	•	54.3	•	•		•			54.3	٠
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ø	N	13	w	14	10	13	N	u	4	10	N	10	s	v	4	4	4	N	11	ü	13	4	٢	
Q9ZX77	Q45916	Q90762	093869	Q69013	022706	042389	066117	P91388	8N9 X 6 O	Q9XFN8	086691	065875	Q27742	061171	Q9Y5H6	075281	075283	Q50288	Q63418	093264	093319	Q15066	057984	CACOKT
NTNH.	138KDA PROTEIN ASSOCIA	CHICKEN CADHERIN-6B.	GLYCOGEN SYNTHASE.	POLYMERASE (FRAGMENT).	F8A5.20 PROTEIN.	SUCRASE-ISOMALTASE (FR	HYPOTHETICAL 16.3 KD P	COSMID K12D9.	CADHERIN-10.	F17F8.5.	PUTATIVE TRANSPORT SYS	CELL DIVISION PROTEIN	GLUTATHIONE PEROXIDASE	CENTRIN 1 (FRAGMENT).	PROTOCADHERIN ALPHA 8.	KIAA0345-LIKE 6.	KIAA0345-LIKE 8.	PUTATIVE LIPOPROTEIN.	PROTOCADHERIN 3.	CADHERIN PRECURSOR.	CADHERIN 11.	OB-CADHERIN-2.	504AA LONG HYPOTHETICA	RECNOCUEAGE BLE.
1.81e+01	1.81e+01	1.81e+01	1.81e+01	1.81e+01	1.81e+01	1.81e+01	1.81e+01	1.18e+01	1.18e+01	1.18e+01	1.18e+01	1.18e+01	1.18e+01	1.18e+01	7.66e+00	7.66e+00	7.66e+00	7.66e+00	7.66e+00	7.66e+00	7.66e+00	7.66e+00	7.66e+00	/. ooe+00

ALIGNMENTS

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(TIEMBLrel. 12, Last HERIN-7. us (Chicken). us (Chicken). Metazoa; Chordata; Cru Galliformes; Phasian:		ULT 2 090763 PRELIMINARY; PRT; 785 AA.	FGIFVVDKNTGDINI	Query Match 85.7%; Score 90; DB 11; Length 993; Best Local Similarity 86.7%; Pred. No. 4.79e-07; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0; 97 FGTFVVDPNNGDINI 111	E 993 AA;	Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat. NON TER 993 993	cadherin; 4.	PROSITE: PS00232: CADHERIN: 2	U86016; AAB65091.1;	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).		STRAIN-BALB/C;	SEQUENCE FROM N.A.	Eutheria; Modentia; Sciuroghathi; Muridae; Murihae; Mus. [1]	; Metazoa;		•	3 (FRAGMENT)	OI-NOV-1996 (TYEMBEREL OS, LAST Sequence update)	(TremBLrel. 05, Creat		O35902 PRELIMINARY; PRT; 993 AA.	RESULT 1

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RESULT 3
IN RESULT 3
IN RESULT 3
IN O76356;
AC 076356;
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Matches
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L Development 121:1321-1332(1995).

C -: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY REMBL; D42150; BAA07721.1; -. REMBL; D42150; BAA07721.1; -. REMSL; PS116; 1NCJ.

R PROSITE; PS0023; CADHERIN; 3. RPFAM; PF00028; Cadherin; 5. RPFAM; PF01049; Cadherin; 5. RPFAM; PF01049; Cadherin. Transmembrane; Calcium-binding; RepRINTS; PR00205; CADHERIN.

Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Rep Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Rep Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Rep
Submitted (MAY-1998) to the EMBL/C
-!- SUBCELLULAR LOCATION: TYPE I N
EMBL; AF067611; AAC19184.1; -.
PROSITE; PS00232; CADHERIN; 1.
PFAM; PF00028; cadherin; 3
Cell adhesion; Glycoprotein; Tran.
SEQUENCE 1329 AA; 146518 MW;
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SEQUENCE FROM N
STRAIN-WHITE LE
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
DANTE M., WAMSLEY P.;
The sequence of C. elegans
Submitted (JUN-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU 2., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA M., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                     WATERSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WATSON A., WEINSTOCK L., WILKINSON SERVER J., TOTAL OF "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE: 94150718.
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C45G7.6.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 368:32-38(1994).
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NAKAGAWA S., TAKEICHI M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhabditina;
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:||::| |||||:
GIFVVDKNTGDIN 14
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12,
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TYPE I MEMBRANE PRO
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EMBL/GenBank/DDBJ
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Pred. No. 1.24e-01;
  Transmembrane;
MW; B161D39E CF
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PROTEIN (BY S:
                         Calcium-binding;
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OSS701;
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O1-NOV-1996 (TrEMBLrel. 01, L
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PROSITE; PS00232; CADHERIN; 25.
PRINTS; PR00205; CADHERIN.
Cell adhesion; Glycoprotein; T
SEQUENCE 3503 AA; 379719 MM
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024292;
01-NOV-1996
01-NOV-1999
01-NOV-1999
                         MEDLINE; 96127529.
KANEKO T., TANAKA A., SATO SUGIURA M., TABATA S.; Sequence analysis of the
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DACHSOUS.
   Synechocystis
                                                                                                                                                       SEQUENCE FROM
STRAIN-PCC6803
                                                                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strain Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                            STRAIN-PCC6803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL 24.5 KD PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLARK H.F., BRENTRUP D., SCHNEITZ K., BIEBER A., GOODMAN C., "Dachbous encodes a member of the cadherin superfamily that imaginal disc morphogenesis in Drosophila."; Genes Dev. 9:1530-1542(1995).
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tacheata; Hexapoda; Insecta;
Etarygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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HSSP; P15116; INCJ.
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Pred. No. 5.11e-01;
2; Mismatches 1
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MW; 16030CA5 CI
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of the unicellular cyanobacterium. I. Sequence features in the 1 Mb
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1.28e+00;
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                                                                                        SAZUKA T.,
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         Query Match
Best Local S
Matches
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MEDLINE: 98049343.

KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E., KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C., FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T., COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOM P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.
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EMBL; D64000; BAA10231.1; -
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KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMUR KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMOTO S., KIMURA T., MIYAJIMA N., HIROSAWA M., SUGIURA M., NAKAZAKI N., NARUO K., OK HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OK SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASU
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TREMBLIFEL 05, 01-JAN-1998 (TREMBLIFEL 05, 101-NOV-1999) (TREMBLIFEL 12, 1) PROBABLE TUNGSTEN-CONTAINING
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Archaea; Euryarchaeota;
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s. 2:153-166(1995).
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  PS00198;
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larity 42.9%;
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  4FE4S_FERREDOXIN;
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MEDLINE: 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., CLAYTON R.A., GOCAYNE J.D.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,

KERLAVAGE A. R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,

OVERBEEK R., KIRKNESS E.F., WEIMSTOCK K.G., MERBICK J.M., GLODEK A.,

SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,

KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
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                              Methanococcus jannaschi
Archaea; Euryarchaeota;
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EMBL; U67574; AAB99349.1; -.
TIGR: MJ1339; -.
                                                                                                                                                                                                                                                                                 Hypothetical SEQUENCE 15
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Archaea; Euryarchaeota; N
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HSSP; P3555; 1EW0.
MEMUREL; 24651, Cucma:1391;24651.
PROSITE: P500010: ASX_HYDROXYL; 1.
PROSITE; P501187; EGF_CA; 1.
Glycoprotein: EGF-11ke domain.
SEQUENCE 624 AA; 69028 MW; AAA97
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033373
033373;
01-JAN-1998 ()
01-JAN-1998 ()
01-AUG-1998 ()
PILC PROTEIN ()
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01-JUN-1998
01-NOV-1999
PV72.
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BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D., KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I., OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A., SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D., UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C., COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORDDOVSKY M., KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus Jannaschil."
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048662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cucurbita maxima (Pumpkin) (Winter squash).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHIMADA T., KUROYANAGI M., NISHIMURA M., HARA-NISHIMURA I.;
"A pumpkin 72-kDa membrane protein of precursor-accumulating vesicles has characteristics of a vacuolar sorting receptor.";
Plant Cell Physiol. 38:1414-1420(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-DEVELOPING COTYLEDON;
MEDLINE; 98182943.
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EMBL; U67573; AAB99343.1; -.
TIGR; MJ1327; -
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2; Mismatches 1
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LACCASE (EC
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SEQUENCE FROM N.A.
STRAIN=GC-653;
MEDLINE; 98129088.
MEDLINE; 98129088.
MEDLINE; 98129089.
"The phase-variable pilus-associated protein PilC is commonly expressed in clinical isolates of Neisserla gonorrhoeae, and sequence variability among strains.";
Microbiology 144:149-156(1998).
EMBL; AJ001121; CAA04547 1; -.
EMBL; AJ001121; CAA04547 1; -.
EMBL; AJ001121; CAA04547 1; -.
                                                                                                                                                                                                                                                                                                                                                                     STRAIN-VC-16 / DSM 4304 / ATCC 49558;

KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,

KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,

KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,

FLEISCHMANN R.D., OUACKENBUSH J., LEE N., SUTTON G.G., GILL S.,

KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.

PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHG

OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTIERBACK T.

COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,

SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,

MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,

VENNTED T.
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                                                                                                                                                                                                                                     PFAM; PF00582; Usp; 1.
Hypothetical protein.
SEQUENCE 270 AA; 29554
                                                                                                                                                                                                                                                                              "The complete genome sequence of the hyperthermophilic, reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL, AE000981; AAB89491.1; ..
HSSP: Q57997; 1MJH.
TIGR; AF1760; ..
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Archaea: Euryarchaeota;
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Submitted (APR-1998) to the EMBL/G
EMBL; AL022537; CAA18582.1; -
MENDEL; 29102; Arath;3426;29102.
Hypothetical protein.
SEQUENCE 593 AA; 68632 MW; 9EA
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BEVAN M., BENES V., RECHMANN S., BORKOVA D., A
MEWES H.W., MAYER K.F.X., SCHUELLER C.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;

core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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MEDLINE: 99115479.
RANOCHA P., MCDOUGALL G., HAWKINS S., STERJIADES R., BORDERIES
STEWART D., CABANES-MACHETEAU M., BOUDET A.M., GOFFNER D.;
"Biochemical characterization, molecular cloning and expression"
"Biochemical characterization, molecular cloning and expression"
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Ropulus trichocarpa (Western balsam poplar).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Popu
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"A STITKING OFGALIZATION OF A LATE
INC. Cell adhesion genes.";

Cell 97:779-790(1999).

-I- SUBCELULAR LOCATION: TYPE I
EMBL; AC005609; AAC34321.1;

EMBL; AC102483; AAD43744.1;

EMBL; AF152483; AAD43744.1;

PROSITE; PS00232; CADHERIN; 5.

PFAM; PF00028; CADHERIN.

R PRINTS; PR000205; CADHERIN.
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MEDLINE: 99308636.

WU Q., MANIATIS T.;

"A STIPLING organization of a large family of human neural cannel c
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KADNER K., MIGUEL T., MILLER C
SUBRAMANIAN S., MARTIN C.H.;
"Sequencing of human chromosom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08738349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08738349 Patent No. 5869638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
Local Similarity 100.0%;
nes 15; Conservation
                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                    NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 0248
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FGIFVVDKNTGDINI 15
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                                                                                                                                                                                                                                                                                    ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
UENCE 15 AA: 1652 MW; 1115 CN:
                              MOLECULE TYPE: peptide
JENCE 615 AA; 67754 MW; 1891114 CN;
                                                                                                                                                                   APPLICATION NUMBER: US 08/112,061 FILING DATE: 26-AUG-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Bone-Related TITLE OF INVENTION: Process for NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                   TOPOLOGY:
                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/738,349 FILING DATE: 25-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                       LENGTH:
                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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1300 I Street, N.W.
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 Score 57; DB 2; I
Pred. No. 3.04e+01;
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Pred. No. 2.01e-04;
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                                     Matches
                                             Query Match
Best Local Similarity
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                                                                            SEQUENCE
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                100 IFVIDDKSGNIH 111
                                                                                                              TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08738349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL
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3 IFVVDKNTGDIN
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                                                                                                                                                       NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                          FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/364,439
APPLICATION NUMBER: US 08/364,439
                                                                                                                                                                                                 FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: Patentin Release (
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Bone-Related TITLE OF INVENTION: Process for NUMBER OF SEQUENCES: 12
                                                                                     MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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CITY: Washington
                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/738,349
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                                                                                                                                                                                                                                       FILING DATE:
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                                                                          LE TYPE: protein 693 AA; 76422 MW;
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                                              54.3%;
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                                   Score 57; DB 2;
Pred. No. 3.04e+01
5; Mismatches
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US-08-738-349-2

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Patent No. GENERAL II Sequence 2,

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Query Match 54.3%;
Best Local Similarity 50.0%;
Matches 6; Conservative
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                                                                                                                                               100 IFVIDDKSGNIH 111
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: BATKET, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                        TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
                                                                                                                     3 IFVVDKNTGDIN 14
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APPLICANT: Okazaki
APPLICANT: Kawai,
APPLICANT: Tsujimu
APPLICANT: Amann,
                                                                                                                                                                                                                        MOLECULE TYPE: protein JENCE 796 AA; 88112 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and TITLE OF INVENTION: Process for Its Production NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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5869638
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E: Dunner
1300 I Street, N.W.
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Takeshita, Sunuc
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Tsujimura, Atsushi
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Pred. No. 3.04e+01;
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Best Local Similarity
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                                                                             Sequence 4, Application US/08738349 Patent No. 5869638
                                                                                                                                                                                                                                                                        100 IFVIDDKSGNIH 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 58, Application US/08188228 Patent No. 5597725 GENERAL INFORMATION:
                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/049
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION UDBER: US 07/872
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5597725and, Greeta E
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 3134
TELECHNOMICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-0448
                                                                                                                                                                                                                                                3 IFVVDKNTGDIN
                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
JENCE 796 AA; 88049 MW; 3168744 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 APPLICANT:
                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NERAL INFORMATION:
APPLICANT: Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (5-3856
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 Sec
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suzuki, Shintaro
VENTION: CADHERIN MATERIALS AND METHODS
EQUENCES: 62
                      Okazaki, Makoto
Kawai, Shinji
Tsujimura, Atsushi
Amann, Egon
                                                  Takeshita, Sunao
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                                                                                                                                                                                                                                                                                                             54.38;
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Pred. No. 3.04e+
5; Mismatches
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SEQUENCE

TOPOLOGY:

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Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 796 AA; 87931 MW; 3173092 CN;
                                                                                                                                                                                                  Sequence 52, Application US/08332643
                                                                                                                                                                                                                                                     XXXXXX
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                                                                                                                                                                         Sequence 52, Application
                                                                                                                                                                                                                                                                                                                                                    100 IFVIDDKSGNIH 111
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FILING DATE: 25-OCT 1996
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE: 26-AUG-1993
ATTORNEY/REENT INFORMATION:
                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              3 IFVVDKNTGDIN 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: BO
TITLE OF INVENTION: Pr
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 202-408-4000
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MEDIUM TYPE: Floppy disk
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                       STREET: Two First National Plaza, STREET: Street CITY: Chicago STATE: Illinois
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REFERENCE/DOCKET NUMBER: 02481.1323-00000
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               COUNTRY:
                                                                         ADDRESSEE:
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                                                                                  Marshall, O'Toole, Gerstein, Murray &
                                                                         Bicknell
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                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                              CADHERIN MATERIALS AND METHODS 56
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                                                                                                                                                                         US/08332643
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Pred. No. 3.04e+01
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                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-332-638-58
  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION UNUBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
FILING DATE: 17 APR 1992
FILING DATE: 17 APR 1992
                                                                                                                                                                                                                                                                                                                                                Sequence 58, Application US/08332638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 IFVIDDKSGNIH 111
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                                                                                                                                                                                                                                                                                                                         Sequence 58, Application US/08332638
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SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: NO. 5639634and, Gr.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Re
CURRENT APPLICATION DATA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/332,643
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Similarity 50.0%;
6; Conservative
                                                                                                                                                           60606
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                                                                                                                                                                                                                                  Marshall, O'Toole, Gerstein, Murray
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Pred. No. 3.04e+01;
5; Mismatches 1
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Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                    ATTORNEY/AGENT INFORMATION:

NAME: Young J. Suh

REGISTRATION NUMBER: P-41,337

REFERENCE/DOCKET NUMBER: 27866/:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEFAX: 312/474-0448

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids

TYPE: HE 179 amino acids
    SEQUENCE
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GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 IFVIDDKSGNIH 111
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                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CITY: Chicago
TMATE: Illinois
TMATE: TISA
  MOLECULE TYPE: protein | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP | STAP 
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein JENCE 796 AA; 88049 MW; 3168744 CN;
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                   TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/
FILING DATE: June 27, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, & ADDRESSEE: Borun
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TELEX: 25-3856
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Pred. No. 3.04e-
5; Mismatches
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Best Local Similarity

Matches 7; Conser
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Best Local Similarity 46.7%;
Matches 7; Conservative
                                        US-08-453-702A-112
                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 797 AA; 87474 MW; 3358246 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XXXXXX
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                                                                                                     288 FOPFVIDEITGEIHL 302
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                                                                                                                                                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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APPLICANT: Suzuki,
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                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: NO. 5708143and, Gr
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,695A
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Protocadherin Materials and Methods NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 233 Sout
CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, & ADDRESSEE: Borun
                                                                                                                                                                                                            LENGTH:
                                                                                                                           Conservative
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                                        STANDARD;
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                                                                                                                       Score 57; Db ., ored. No. 3.04e+01;
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Query Match 54.3%;
Best Local Similarity 46.7%;
Matches 7; Conservative
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                                                                                                                                                                                    Sequence 112, Application PC/TUS9508071
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                                                                                                                                                                                                                                                                      PCT-US95-08071-112
                                                                                                                                                                                                                                                                                                                                                 288 FOPFVIDEITGEIHL 302
                                                                                                                                          Sequence 112, Application PC/TUS9508071 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          | ||:| ||:|::
1 FGIFVVDKNTGDINI 15
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Protocadherin Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: NO. 5891706and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
TELEPHONE: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
JENCE 797 AA; 87474 MW; 3358246 CN;
                                                                                       APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocac
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 233 Sout
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marsh
ADDRESSEE: Borun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                    STREET: 6300 Sea
CITY: Chicago
STATE: Illinois
                                                              ADDRESSEE:
        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08453702A
60606
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                                                  6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marshall, O'Toole, Gerstein, Murray,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                  Borun
                                                                            Marshall, O'Toole, Gerstein, Murray,
                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                       protocadherin Materials and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/453,702A
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Matches
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Noland, Greta E.
REGISTRATION NUMBER: 3214
REFERENCE/DOCKET NUMBER: 3214
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08472481 Patent No. 5863804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 54.3%;
Local Similarity 46.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US93/12588 FILING DATE: 23 DEC 1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/998,003 FILING DATE: 29 DEC 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
JENCE 797 AA; 87474 MW; 3358246 CN;
                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,481
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                             MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US95/08071
                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                  CITY: San Diego
                                                                                                                                                                                                                 STREET:
                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                              ADDRESSEE:
        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                     E OF INVENTION:
                                                                                                                                                           92122
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            US 08/213,361
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9901
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE 837 AA; 92281 MW; 3540645 CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-474-067-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08474067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 GIFIIERETG 168
           TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,361
EILING DATE: 14 -MAY 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/607,293
EILING DATE: 30-0CT 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.38;
Local Similarity 50.08;
les 5; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GIFVVDKNTG 11
                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadherin Adhesion Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                APPLICATION NUMBER: US/08/474,067 FILING DATE: 07-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 14-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                               92122
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                                                                                                                                                                                                                                                                                                        California
: United States
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4370 La Jolla Village Drive,
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30-OCT-1990
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Pred. No. 3.04e+01;
5; Mismatches n
                                                         P-LJ
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                           159 GIFIIERETG 168
                                                   Local Similarity
les 5; Conser
     2 GIFVVDKNTG
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REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08474068A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08474068A Patent No. 5837525
                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/21
FILING DATE: 14-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/60
FILING DATE: 30-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 54.3%;
Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/474,068A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GIFVVDKNTG
                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 837 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: STREET: STREET: SAN DIEGO
CTATE: California
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ranscht, Barbara
TITLE OF INVENTION: T-Cadhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: ami
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                                                                 .OGY: linear
837 AA; 92281 MW; 3540645 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States
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30-OCT-1990
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Score 57; DB 2;
Pred. No. 3.04e+01
5; Mismatches
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                               Length 837
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp Run on: protein - protein database search, using Smith-Waterman algorithm Sat May 13 07:10:47 2000; MasPar time 3.01 Seconds 117.892 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-991-628-3 (1-15) from US08991628.pep 96

1 LNSKIAFKIVSQEPA 15

Scoring table: PAM 150 Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 18.170; Variance 51.971; scale 0.350

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Score	Query Match	Length	BG	ID	Description	Pred. No.
ц.	96	100.0	15	۱ -	W04843	Self epitope of desmoq	3.93e-04
2	96		15		8	oglein-3 190	3.93e-04
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0	87	90.6	778		W15489	igus foliaceus a	5.50e-03
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11	54	•	2233		W48711	ര	•
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14	53		456	۲	W82841	Human cerebral protein	
15	49	•	572	۳	R40843	Bilirubin oxidase.	. 7:
16	49	•	916	μ	W13129	Full length human cadh	. 7
17	49	•	916	Ь	W25658	ч	
18	49	•	2408	Н	R24307	Translation of ORF 3 c	. 7
19	48	50.0	26		W60192	ಕ್ಷ	N
20	48	50.0	528	۳	W20908	H. pylori inner membra	N
21	48	50.0	2016	ب ــو	W23994	sodium	N
22	48	50.0	2019	_	R67913	Cardiac sodium channel	2.25e+02
23	48	50.0	2020	ja	R06584	Cardiac sodium channel	2.25e+02

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Query Match 100.0%; Best Local Similarity 100.0%; Matches 15; Conservative

Score 96; DB 1; Length 15; Pred. No. 3.93e-04; 0; Mismatches 0; Indels

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45	44	43	42	41	40	39	38	37	36	<u>3</u> 5	34	ω ω	32	31	30	29	28	27	26	25	*
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R35199	R13516	R99579	R98226	W38455	W34554	R13498	Y07080	R97628	R97631	R97630	R97629	W79334	R97246	R30177	R30730	R75731	R75741	W74883	W89745	W75006	XCOO45
Mouse multidrug resist	P.denitrificans COB N.	Calpain large subunit	Rat neuronal protein k	Yeast RNA-binding prot	MilTL glycosidase 29G.	P.denitrificans COB G.	-	Human SLAM1 T-cell co-		Human SLAM3 T-cell co-	Human SLAM2 T-cell co-	Staphylococcus aureus	Virulence gene cluster	PPI.	B. burgdorferi 79 kD a	B. burgdorferi strain	B31 outer surface prot	Human secreted protein	Staphylococcus aureus	Human secreted protein	mamarian growen normon
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PS Disclosure; Column 4; 42pp; English.

CC The patent describes a new preparation of microparticles each CC comprising a polymeric matrix and a nucleic acid. The polymeric CC matrix consists of one or more synthetic polymers having a solubility CC in water of less than 1 mg/l (e.g. poly-lactic-co-glycolic acid);

CC and at least 90% of the microparticles have a diameter of less than CC 100 microns. The microparticles are useful for the delivery of nucleic acids to phagocytic cells. In one embodiment the microparticles are cells to phagocytic cells. In one embodiment the microparticles are colored circular form) includes an expression control sequence CC coperatively linked to a coding sequence, where the expression product CC of the coding sequence is a polypeptide having a length and a sequence CC which permits it to bind to an MHC class I or I molecule. The cepression product is thus an effective stimulator of an immune CC expression by the nucleic acid. It is associated with pemphigus
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Best Loc
Matches
                                                                                                                                                                         23-JUL-1998.
22-JAN-1998; U01499.
06-JAN-1998; US-003253.
22-JAN-1997; US-787547.
(PANG-) PANGAEA PHARM INC.
gene therapy gene; Page 8; 101pp; English.
Disclosure; Page 8; 101pp; English.
A microparticle preparation (MP) has been developed, consisting of a microparticle having a diameter of less than 100 mu m. The MP comprises:
(a) a polymeric matrix (PM) consisting of one or more synthetic polymers a polymeric matrix (PM) consisting of one or more synthetic polymers.
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Curley JM, Hedley ML, Langer
WPI; 98-427077/36.
                                                                                gene therapy
Disclosure; Page
                                                                                                            New preparations of microparticles matrix and nucleic acid comprising
                                                                                                                                               Curley JM, Hedley ML, WPI; 98-427556/36.
                                                                                                                                                                                                                                                                                                Desmoglein 3 protein fragment 190-204.
Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen; class II associated peptide; pathogen; gene therapy; genetic disease; infection; downregulation; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desmoglein-3 190-204. Desmoglein; DG; gene therapy; pemphigus vulgaris; microparticle; autoantigen; autoimmune disease; MHC.
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US5783567-A.
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CR Also described is a MP of at most 20 microns in diameter, comprising: (a) a PM; and (b) a NAM comprising an expression control sequence operatively clinked to a coding sequence, where the coding sequence encodes an correct expression product selected from: (l) a polypeptide at least 7 amino conditions and the sequence of: (l) a class in length, having a sequence identical to the sequence of: (l) a fragment of a naturally-occurring mammalian protein; or (ii) a fragment correct in a naturally-occurring mammalian protein; or (ii) a fragment correct in a mammal; (2) a peptide having a length and sequence which infects correct to an MRC class I or II molecule; and (3) the polypeptide or the CC bind to an MRC class I or II molecule; and (3) the polypeptide or the correct into phagocytic cells. They can be used for gene therapy, e.g. for the antimer presence.

CC to preating genetic diseases, infections or tumours or for downregulating correct corrections.
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pemphigus
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fused protein recognised by pemphigus vulgaris auto:antibody - useful to treat and diagnose pemphis vulgaris Claim 1; Page 7-9; Ppp; Japanese.

W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients wit pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, interpolermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgG1 hinge region and the resulting fusion protein is useful to treat or diagnose
                                                                                                                                     R30742
R30742;
                                                Human pemphigus vulgaris 130kD antigen.
Pemphigus vulgaris; skin disease; autoantibodies;
                                                                                                   14-JUN-1993 (first entry)
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30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
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J08188540-A.
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                                                                                                                                                                                                                                                                                                                                                                    remphigus follaceus antigen-IgG constant region fusion protein - linked through the hinge region used to treat pemphigus follaceus Claim 1; Page 10-12; 17pp; Japanese.
Claim 1; Page 10-12; 17pp; Japanese.
Claim 1; Page 10-12; 17pp; Japanese.
Constant to the extracellular recognised by pemphigus foliaceus patient autoantibody which comprises the constant region of IgG linked to the extracellular region. Pemphigus foliaceus is antigen protein through the hinge portion. Pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus follaceus. The antigen is especially administered through an adsorbent upon which the fusion protein is immobilised via a carrier. The fusion protein is also useful for detecting pemphigus follaceus antibodies which is useful in immunodiagnosis. The fusion protein has little or no side effects.
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15-DEC-1992:
27-NOV-1991: 798918.
27-NOV-1991: US-798918.
(USSH ) US DEPT HEALTH & HUMAN SERVICE.
Amaga1 M, Klaus-Kovtun V, Stanley JR;
WPI; 93-067436/08.
N-PSDB: 035992.
  W13010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J09077800-A.
25-MAR-1997.
12-SEP-1995;
12-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W15489;
W15489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding pemphigus vulgaris antigen - useful in proteins for diagnostic and therapeutic uses Disclosure; Fig 7; 50pp; English.
This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment pemphigus vulgaris. It is thought that the antigen may be a cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUN-1997 (first entry)
Pemphigus foliaceus antigen-IgG constant region fusion protein.
Pemphigus foliaceus; autoantibody; constant region; IgG;
Pemphigus foliaceus; autoantibody; constant region; IgG;
extracellular region; antigen; hinge portion; skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; T66428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NISH/) NISHIKAWA '
WPI; 97-241758/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dermatitis herpetiformis; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adhesion molecule.
Sequence 999 AA;
                                                                                                                                                                                   190 LNSKIAFKIIRQEPS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 LNSKIAFKIVSQEPA 204
                                                                                                                                                                                                                                                                  Local :
                                                                                                                                                                                                                                                                                                                                                immunodiagnosis.
quence 778 AA;
                                                                                                                                   -
                                                                                                                                 LNSKIAFKIVSQEPA
                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                         Similarity
12; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 100.0%;
Similarity 100.0%;
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                         90.6%;
larity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260899.
JP-260899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens.
                         protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Pemphigus foliaceus antigen protein"
                                                                                                                                                                                                                                         Score
Pred.
2; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
0; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             re 96; DB 1; Le
d. No. 3.93e-04;
Mismatches 0;
                                                                                                                                                                                                                                         re 87; DB 1; I
1. No. 5.50e-03;
Mismatches I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection; ss.
                                                                                                                                                                                                                                                                                        Length 778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell
                                                                                                                                                                                                                                                                                                                                                                          effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                         Gaps
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RESULT PRESULT    PF 23-AUG-1995; 031033.

PR 23-AUG-1995; DE-031033.

PR 23-AUG-1995; DE-031033.

PR 23-AUG-1995; DE-031033.

PR (PROG-) PROGEN BIOTECHNIK GMBH.

PI Franke WW, Schaefer S;

PR (PROG-) PROGEN BIOTECHNIK GMBH.

PI Franke WW, Schaefer S;

PR WPI; 97-146518/14.

PT surface of epithelial or carcinoma cells, not bound to desmosomes, experiment for diagnosis and treatment of carcinoma micrometastases.

PT useful for diagnosis and treatment of the desmosomal cadherin (DC), carcinoma cells and not bound to desmosomes.

PS Claim 7; Page 5; Bpp; German.

CC The present sequence is a segment of the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab)

CC desmoglein Dsg2, which is exposed on the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab)

CC diagnose, i.e. to detect carcinoma cells, especially

CC diagnose, i.e. to detect carcinoma cells, especially

CC diagnose, i.e. to detect carcinoma cells by cell sorting methods and care to liver agents, e.g. other Ab or toxins, to compare the cells. The Ab provides rapid and reliable detection of metastatic carcinoma, and detects parts of DC that are not more and tissue or carcinoma cells. Basin normal tissue or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
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PR 23-AUG-1995; DE-031033.
PR (PROG-) PROGEN BIOTECHNIK GMBH.
PI Franke WW, Schaefer S;
PR Antibody reactive with part of desmosomal cadherin - exposed on PT surface of epithelial or carcinoma cells, not bound to desmosomes, PT useful for diagnosis and treatment of carcinoma micrometastases PS Claim 9; Page 5; Bpp; German.
CC The present sequence is a segment of the desmosomal cadherin (DC).
CC desmoglein Dag2, which is exposed on the surface of epithelial or CC diagnose, i.e. to detect carcinoma cells, especially
CC discreted against epitopes of the present sequence can be used to CC diagnose, i.e. to detect carcinoma cells, especially
CC micrometastases, not bound to desmosomes, to separate, enrich or CC detect living or fixed carcinoma cells, especially
CC micrometastases, not bound to desmosomes, to separate cells. The Ab provides rapid and reliable detection of CC arcessible in desmosome bound cells, as in normal tissue or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Segment of desmosomal cadherin, desmoglein Dsg2.
Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithelial;
carcinoma; desmosome; antibody; epitope; diagnosis; detection;
micrometastasis; separation; enrichment; targetted delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Segment of desmosomal cadherin, desmoglein Dsg2.
Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithelial; carcinoma; desmosome; antibody; epitope; diagnosis; detection; micrometastasis; separation; enrichment; targetted delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE19531033-A1.
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DE19531033-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W13009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 LNSKISYRIVSLEPA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LNSKIAFKIVSQEPA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 73.3%
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Pred. No. 9.0
3; Mismatcl
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ဝူ
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PI MOTROW JS, Rimm DL;

PI G. 18426/22.

DR NPSDB; 065487.

DR N-PSDB; 065487.

DR N-PSDB; 065487.

PT develop prods. for diagnosis, prognosis, therapy and prophylaxis of t-cadherin disorders, e.g. mallgnancies

PT develop prods. for diagnosis, prognosis, that is also known as claim 1: page 59-63; 97pp; English.

CE treadherin is a cell adhesion molecule that is also known as claim 1: page 59-63; 97pp; English.

CE treadherin is a colonic epithelia cell CNA ilbrary. The following sequences and a colonic epithelial cell CNA ilbrary. The following components and a colonic epithelial cell CNA ilbrary. The following sequences are specifically claimed: AAs 1-878; 151-878; 30

CE sequences are specifically claimed: AAs 1-878; 151-878; 30

CE 401; AAS 402-51; AAS 178-51; AAS 1-50; AAS 178-289; AAS 290-

CE 401; AAS 402-51; AAS 178-51; AAS 1-50; AAS 1-703; AAS 728-878;

CE 401; AAS 402-51; AAS 178-51; AAS 151-703; AAS 1-703; AAS 728-878;

CE 401; AAS 402-51; AAS 151-2696; 1332-3000; 540-1500; 348-906; 890-

CE 2749; 566-2749; 1-1053; 510-2696; 1332-3000; 540-1500; 348-906; 890-

CE 2749; 566-2749; 1-1053; 510-2696; 1332-3000; 540-1500; 348-906; 890-

CE 2749; 566-2749; 1-1053; 510-2696; 1332-3000; 540-1500; 348-906; 890-

CE 2749; 566-2749; 1-1053; 510-2696; 1332-3000; 540-1500; 348-906; 890-

CE 2749; 566-2749; 1-1053; 510-2696; 1332-3000; 540-1500; 348-906; 890-

CE 2749; 566-2749; 1-1053; 510-2696; 1332-3000; 540-1500; 348-906; 890-

CE 2749; 566-2749; 1-1053; 510-2696; 1332-3000; 540-1500; 348-906; 890-

CE 2749; 566-2749; 1-1053; 510-2696; 1332-3000; 540-1500; 348-906; 890-

CE 2749; 566-2749; 1-1053; 510-2696; 1332-3000; 540-1500; 348-906; 890-

CE 2749; 566-2749; 1-1053; 510-2696; 1332-3000; 540-1500; 348-906; 890-

CE 2749; 566-2749; 1-1053; 510-2696; 1332-3000; 540-1500; 348-906; 890-

CE 2749; 566-2749; 1-1053; 510-2696; 1302-3000; 540-1500; 348-906; 890-

CE 2749; 568-2
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches
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Best Local Similarity
Matches 11; Consei
                                                                                                                                                  Human E-cadherin precursor.
E-cadherin; T-lymphocyte; a
autoimmune disease; Crohn d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-1994 (first entry)
Sequence of human liver E-cadherin.
Human epithelial-cadherin; E-cadherin; cell adhesion molecule;
uvomorulin; L-CAM; Cell CAM 120/80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carcinomas.
Sequence
                                                                                                                                                                                                                              R85487 standard;
R85487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R55060 standard: Protein;
R55060;
08-NOV-1994 (first entry
                                                                                                   peptide
                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-NOV-1993;
17-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9411401-A.
26-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                               18-MAR-1996
                                                                                                                                                                                                                                                                                                                                                               293
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                                                                                                                                                                                                                                                                                                                          N
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                                                                                                                                                                                                                                                                                                                                                               NAAIAYTILSQDP
                                                                                                                                                                                                                                                                                                                          NSKIAFKIVSQEP
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                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        560
                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               56.3%;
larity 53.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                            1. .150
/label-
/label= Extracellular_domain
/note= "the extracellular domain (amino acids
of the mature protein) is the preferred
                                                                                                                                                                                                                                                  Protein;
                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 2
8
8
                                                                            Sig_peptide
                                                                                                                                                      alpha-E, beta-7 integrin;
disease; psoriasis.
                                                                                                                                                                                                                                                  878
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                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
4; M
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Pred.
3; M
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                                                                                                                                                                                                                                                                                                                                                                                               e 54; DB 1; Le
. No. 4.96e+01;
Mismatches 2;
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; I
9.68e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 878;
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Best Local S
Matches
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13-OCT-1998 (first entry)
HPIV-3 JS isolate wild-type L protein.
L protein; attenuation; non-segmented; negative
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09-NOV-1995:
03-MAY-1995;
03-MAY-1994;
                                                                                                           Recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of order Mononegavirales - having attenuating mutation in 3' genomic promoter region and RNA polymerase gene, useful as vaccine to immunise against such virus Disclosure; Page 246-254; 426pp; English.

This sequence represents the wild-type L protein from Human parainfluenza virus (HPIV-3) type 3 isolate JS. This sequence is used in a method which involves the isolation of recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of the order Mononegavirales which have at least 1 attenuating mutation in the 3' mononegavirales which have at least 1 attenuating mutation in the 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BGHM ) BRIGHAM & WOMENS HOSPITAL Brenner MB, Cepek KL; WPI; 95-92921/50.
genomic promoter region and at least
polymerase gene. This RNA virus can b
individual against such a virus.
Sequence 2233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMCY ) AMERICAN CYANAMID CO.
(USSH) US DEPT HEALTH 6 HUMAN SERVICES.
MUZDHY BR, Randolph VB, Sidhu MS, Tatem
WPI; 98-230710/20.
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19-SEP-1997; U16718.
27-SEP-1996; US-026823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human parainfluenza virus.
WO9813501-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W48711 standard;
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The human E-cadherin protein precursor (R85487) is an cDNA clone (T05764) derived from human liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting adhesion isolating agents to psoriasis, etc
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727. .876
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No. 4.96e+01
                                                          t 1 attenuating mutation be used as a vaccine to
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Query Match Best Local s Matches

Similarity 5; Conser

56.3%; larity 33.3%; Conservative

Score 54; DB 1; I Pred. No. 4.96e+01; 7; Mismatches

Length 2233;

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Gaps

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LNSKIAFKIVSQEPA LDRSVLYRIMNQEPG

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Best Local
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19-SEP-1997; U5-026823.
27-SEP-1996; US-026823.
(AMCY ) AMERICAN CYANAMID C (USSH) US DEPT HEALTH & HU MULTPHY BR, RANDOLPH VB, S1d WPI; 98-230710/20.
N-PSDB; V18273\.
Recombinantly-generated, attenuated, non-segmented negative-sense, single stranded RNA virus of order Mononegavirales - having attenuating mutation in 3' genomic promoter region and RNA polymerase gene, useful as vaccine to immunise against such virus plsclosure; Page 265-273; 426pp; English.

This sequence represents the Human parainfluenza virus (HPIV-3) type vaccine FRAI cp45 L protein. This sequence is used in a method which involves the isolation of recombinantly generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of the order
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W48712 standard; Protein: 2233 AA.
W48712;
W48712;
13-OCT-1998 (first entry)
HPIV-3 FRh1 cp45 vaccine L protein.
L protein: attenuation; non-segmented; negative sense; vaccine; immunity;
single stranded RNA virus; Mononegavirales.
W03813501-A2.
W03813501-A2.
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19-SEP-1997; U16718.
27-SEP-1996; US-026823.
(AMCY ) AMERICAN CYANAMID CO.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
MULPHY BR. RANDOLPH VB, SIDHN MS, Tatem
WPI: 98-230710/20.
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W48713;
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Pred. No.
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Matches
24-JAN-1992; 034126.
24-JAN-1992; JP-034126.
(AMAN ) AMANO PHARM KK.
WPI; 93-284681/36.
WPSDB; 047790.
Bilirubin oxidase prepn. usefuculturing bilirubin oxidase ir Claim 1; Page 29-32; 32pp; Jag
                                                                                                                                                                                                              10-AUG-1993.
24-JAN-1992;
24-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bilirubin; oxidase; analytical; polymerase chain reaction. Myrothecium verrucaria.
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for treating ischaemic brain diseases and nerve denaturation
conditions such as Parkinson's and Alzheimer's diseases
Claim 1; Fig 4; 17pp; Japanese.
The present sequence represents human cerebral protein-1 (HUCEP-1 has neuron function activating activity. HUCEP-1 is ufor treating ischaemic brain diseases and nerve denaturation
conditions such as Parkinson's and Alzheimer's diseases.
Sequence 456 AA;
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R40843 standard; Protein;
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03-FEB-1999
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J10257891-A.
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function activating activity; nerve denatured
son's disease; Alzheimer's disease.
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4; Mismatches 1
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Pred. No. 4.96e+01
7; Mismatches
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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Sat May 13 07:10:21 2000; MasPar time 4.28 Seconds 165.192 Million cell updates/sec

Sequence: Description: Perfect Score: >US-08-991-628-3 (1-15) from US08991628.pep 96 1 LNSKIAFKIVSQEPA 15

Tabular output not generated.

Scoring table: PAM 150 Gap 15

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

pir62 1:pirl 2:pir2 3:pir3 4:pir4

Database:

Statistics: Mean 25.750; Variance 32.305; scale 0.797

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ZLNZSE	IJCHCL	T07172	ZLNZP3	S64402	IJMSCN	\$43064	IJHUCE	IJBOCN	T05921	F70126	IJEFTM	S64146	S74520	S49752	IJHUCN	S34438	IJMSCE	T02501	S38673	IJHUG1	IJBOG1	IJHUG3	ID	
genome polyprotein -	E-cadherin precursor	subtilisin-like prote	genome polyprotein -	probable transcriptio	N-cadherin precursor,	cadherin - African cl	_	N-cadherin precursor	N-carbamyl-L-amino ac		cadherin-related tumo		-	homeotic protein YOX1	ğ	uvomorulin - mouse	'n	al pr	in 2	_	desmoglein 1 precurso	desmoglein 3 precurso	Description	
1.09e+01	1 000+01	1.09e+01	7.00e+00	7.00e+00	7.00e+00	7.00e+00	7.00e+00	7.00e+00	7.00e+00	4.45e+00	1.77e+00	1.77e+00	1.11e+00	6.90e-01	27e	4.27e-01	4.27e-01	. 63e			ሞ	1.15e-09	Pred. No.	

45	44	43	42	41	40	39	38	37	36	ω G	34	33	32	31	30	29	28	27	26	25	24
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52.1	52.1	52.1	52.1	52.1	52.1	52.1	53.1	53.1	53.1	53.1	53.1	53.1	53.1	53.1	53.1	53.1	54.2	54.2	54.2	54.2	00.2
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<u>بــ</u>	N	N	N	N	N	N	N	N	N	N	w	2	N	N	N	N	Н	ب	N	N	-
JQ1948	T13481	T02292	A71662	T15203	JC5284	S25314	T13947	T13945	T13949	D72067	T02672	A49341	G64938	E42284	F49846	S63634	B34488	IJCHCB	A71266	C72411	ZLNZSV
	hypothetical protein	hypothetical protein	sodium/pantothenate s	hypothetical protein	carbonyl reductase (N	aspartic proteinase i	neurofibromin - fruit	neurofibromin - fruit	neurofibromin - fruit	polymorphic membrane	hypothetical protein	isocitrate dehydrogen	hypothetical protein	protein -	spa33 protein - Shige	ribosomal protein S3	calpain (EC 3.4.22.17	B-cadherin precursor	probable transcriptio	Holliday junction DNA	genome polyprotein -
4.01e+01	4.01e+01	4.01e+01	4.01e+01	4.01e+01	4.01e+01	4.01e+0	2.62e+01	2.62e+01	2.62e+01	2.62e+01	2.62e+01	2.62e+01	2.62e+01	2.62e+01	2.62e+01	2.62e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01	1.09e+0

ALIGNMENTS

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CLASSIFICATION
KEYWORDS
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#journal Blochem. Blophys. Res. Commun. (1990) 173:1224-1230

#title Desmoglein shows extensive homology to the cadherin

cell adhesion molecules.

#cross-references MUID:91097553
                                                                                                                                                                                     #cross-references MUID:91168965
#accession A48173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors
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                                                                                    ##residues 44-1001,'AQPPSAT' ##label KO3
##cross-references GB:X57784
##note this sequence has been revised
$38721
                                                                                                                                                                ##molecule_type mRNA
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##cross-references EMBL:X57784; NID:g436061; PIDN:CAA40930.1;
PID:g436062
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##residues 44-1
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1-87;968-1043 ##label KO2
##cross-references GB:S64268; GB:S64270
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Eur. J. Cell Biol. (1990) 53:1-12
Identification of desmoglein, a constitutive desmosomal glycoprotein, as a member of the cadherin family of c
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  #superfamily cadherin;
calcium binding; cell #
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S14603
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ir. J. Cell Biol.
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repeat homology duplication; glycoprotein;
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PIDN:AAA62709.1; PID:g552318
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Matches 1
                                                                                                                                    #Journal J. Cell Sci. (1991) 99:809-821
#title Structural analysis and expression of human
#cross-references MUID:92121251
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##residues 26-1049 ##label NIL
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Local Similarity 80.0%;
hes 12; Conservative
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S16906
Wheeler, G.N.; Buxton, R.S.; Parker, A.E.; Rees, D.A.; King, I.A.; Magee, A.I.
                                                      A61279
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desmoglein 1 precursor - human
desmosomal glycoprotein I
*formal_name Homo sapiens *common_name man
30-Jun-1993 *sequence_revision 30-Jun-1993
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#domain extracellular *status predicted *label EXT\
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#domain cadherin repeat homology *label CR2\
#domain cadherin repeat homology *label CR3\
#domain cadherin repeat homology *label CR3\
#domain cadherin repeat homology *label CR4\
#domain transmembrane *status predicted *label TMM\
#domain intracellular *status predicted *label INT\
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                             Arnemann,
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#map_position 18q12:1-18q12:2

CLASSIFICATION #superfamily cadherin; cadherin

KEYWORDS calcium binding; cell adhesion;
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                                            #authors Koch, P.J.; Goldschmidt, M.D.; Walsh, M.J.; Zimbelmann, 1
Franke, W.W.
#journal Eur. J. Cell Biol. (1991) 55:200-208
#title Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second ty of desmoglein gene.
#cross-references MUID:92037656
#accession B38872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    969-1019
110,180
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                                                                                                                                                                                                                                                                                                                                            #accession
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  **molecule_type mRNA
**residues 777-1117 **label
                                                                                                                                                                                                                                                                        ##status preliminary
##molecule_type mRNA
##residues 1-1117 ##label ZIM
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##residues 1-55 ##label WH3
                                                                                                                                                                                                                                                        **cross-references EMBL: Z26317; NID: g416177; PIDN: CAA81226.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 90.6%;
Local Similarity 80.0%;
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S38673
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20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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Desmosomal glycoproteins I, II and III: novel members
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#domain propeptide *status predicted *label PRO\
#product desmoglein *status predicted *label MAT\
#domain extracellular *status predicted *label EXT\
#domain cadherin repeat homology *label CR1\
#domain cadherin repeat homology *label CR2\
#domain cadherin repeat homology *label CR2\
#domain cadherin repeat homology *label CR3\
#domain cadherin repeat homology *label CR3\
#domain cadherin repeat homology *label CR3\
#domain cadherin repeat homology *label CR4\
#region serine/threonine-rich\
#region serine/threonine-rich\
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#domain desmoglein repeat #label DG1\
#domain desmoglein repeat #label DG3\
#domain desmoglein repeat #label DG3\
#domain desmoglein repeat #label DG4\
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Pred. No. 2.27e-07
2; Mismatches
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duplication; glycoprotein;
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161-271
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*map_position 18q12:1-18q12:2

CLASSIFICATION *superfamily cadherin: cadherin

KEYWORDS calcium binding; cell adhesion;
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REFERENCE
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Best Local Similarity 40.0%;
Matches 6; Conservative
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Best Local
                   #journal #title
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#introns 52/2; 107/1; 148/2; 191/3; 212/2; 1317/3; 1346/3
#note T19C21.7
                                                                                   #authors
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Local Similarity 73.3%;
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T02501
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Take1chi, M. Take1chi, M. Take1chi, M. Sature (1967) 329:341-343
Transformation of cell adhesion introduced E-cadherin cDNA.
                                                                                                       S04528; S03160; I49565; S48735
S04528
                                                                                                                                                                  #formal_name Mus musculus #common_name house mouse 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_cl
                                                                                                                                                                                                              uvomorulin
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E-cadherin precursor, epithelial - mouse
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                                                                               Nagafuchi, A.; Shirayoshi, Y.;
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#domain cadherin repeat homology #label CR2
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Pred. No. 2.63e-01
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Pred. No. 6.37e-05;
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##cross-references GB:M81449; NID:g192325; PIDN:AAA37352.1; PID:g192326
REFERENCE S48735
                                                                    SUMMARY
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Query Match
Best Local Similarity
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702-733
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489-597
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157-884
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"Taketchi, M.; Ikura, M.

#journal FEBS Lett. (1994) 352:318-322

#title Purification and spectroscopic characterization of a recombinant anino-terminal polypeptide fragment of mouse epithelial cadherin.

#cross-references MUID:95010732

#accession $48735
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Cadherins mediate calcium-dependent intercellular adhesion, and thought to be involved in the sorting of different cell types
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Lottspeich, F.; Engel, J.; Doelz, R.; Jaehnig, F.; Ep
J.; Mayer, S.; Mueller, C.; Kemler, R.
EMBO J. (1987) 6:3647-3653
The structure of cell adhesion molecule uvomorulin. Ins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #superfamily cadherin; cadherin repeat homology
calcium binding; cell adhesion; duplication; glycoprotein;
transmembrane protein
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The E-cadherin promoter: Functional analysis of a G-C-rich region and an epithelial cell-specific palindromic regulatory element.
                                                                  #length
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#domain cadherin repeat homology #label CR1\
#region cadherin binding #status predicted\
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#domain cadherin repeat homology #label CR3\
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#domain transmembrane #status predicted #label INT\
#domain intracellular #status predicted #label INT\
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*domain propeptide *status predicted *label PRO\
*product E-cadherin, epithelial *status experimental
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#binding_site carbohydrate (Asn)
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                                                                                        predicted
62.5%;
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Score
Pred.
60; DB 1; I
No. 4.27e-01;
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Best Local Similarity 61.5%;
Matches 8; Conservative
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#title The structure of the gene coding for the mouse cell adhesion
#cross-references MUID:92093614
#accession S3443B
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                  #authors
                                                                                                                       #authors Reid, R.A.; Hemperly, J.J.
#Journal Nucleic Acids Res. (1990) 18:5896
#title Human N-cadherin: nucleotide and c
#cross:references.MUID:91016946
                                                                                                                                                                                                                                                         #accession
                                                                                                                                                                                                                                                                        #authors
#submission
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                                              ##note
                                                                                                                                                                                                      ##cross-references EMBL:X54315; NID:g34998; PIDN:CAA38213.1; PID:g34999
                                                                                                                                                                                                                                     ##molecule_type mRNA
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##note the nucleotide sequence was
Library, August 1992
                                                     ##molecule_type mRNA
1-340,'N',342-698,'R',700-704,'F',706-906 ##label RE2
##presidues 1-340,'N',342-698,'R',700-704,'F',706-906 ##label RE2
##pross-references_EMBL:X54315
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N-cadherin; neuronal cadherin
#formal_name Homo sapiens #common_name man
30-Jun-1993 #sequence_revision 30-Jun-1993
22-Jun-1999
Walsh, F.S.;
D.; Spurr,
                               JQ0751
                                                                                                                                                                                                                                                                                                     A38870; S11487; J00751; S13799
A38870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16/3; 57/1; 131/3; 179/3; 231/3; 280/1; 338/3; 524/2; 573/1; 648/1; 724/1; 767/3; 815/3 #superfamily cadherin; cadherin repeat homology
                                                                                                                                                                                                                                                         A38870
                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library,
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R.A.
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translation not shown
                                              this sequence has been revised in reference A38870
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 Barton, C.H.; Putt, N.; Goodfellow, P.N
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Pred. No. 4.27e-01
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                S.E.; Kelsell,
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160-906
160-716
162-267
237-242
270-382
285-497
500-605
606-712
715-746
                                                                                         #journal #title
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#accession S49752
##molecule_type DNA
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                                       #accession $33388
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190,273,325,402,
572,622,651,692
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##molecule_type mRNA
##residues 160-194,'IR','197-211,'L',213-227,'O',229,'N',231-235,
##residues 'G',237-248,'T',250-356,'N',358-530,'KYL',533-906
                                                                                                                   #authors
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ap_position 18q12.1-18q12.1
IFICATION #superfamily cadherin; cadherin repeat homology
RDS calclum binding; cell adhesion; duplication; glycoprotein;
transmembrane protein
                                                                                                                                                                                           ##residues
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TO Cadherins mediate calcium-dependent intercellular adhesion and a thought to be involved in the sorting of different cell types during morphogenesis.
                       ##molecule_type
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Similarity 46.7%;
                                                                                                                                                                                                                                                                                                     Kaufmann, E.
Chromosoma (1993) 102:174-179
In vitro binding to the leucine tRNA
yeast homeobox gene.
nces MUID:93209080
                                                                                                                                                                                                                            submitted to 
$49752
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N-cadherin gene maps
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#domain propeptide #status predicted #label PRO\
#product N-cadherin #status predicted #label EXT\
#domain extracellular #status predicted #label EXT\
#domain cadherin binding #status predicted\
#domain cadherin binding #status predicted\
#domain cadherin repeat homology #label CR2\
#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR5\
#domain transmembrane #status predicted #label INT\
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#corion corion for the predicted #label INT\
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1-290,'QGLIIP'
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ces EMBL: 246659; NID: g575680;
PID: g575692; MIPS: YML027w
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Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.;

Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;

Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo,

S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;

Yasuda, M.; Tabata, S.;

#Journal DNA Res. (1996) 3:109-136

#title Cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

#cross-references MUID:97061201

#accession $74520
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PIDN:BAA16672.1; PID:d1017405; PID:g1651744
##note the nucleotide sequence was submitted to the Elibrary, June 1996
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##residues 1-1:
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Similarity 63.6%;
7; Conservative
            cerevisiae)
hypothetical protein G2842
#formal_name Saccharomyces cerevisiae
17-May-1996 #sequence_revision 17-May-1996
17-Apr-1998
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#length 138 #molecular-weight 16580 #che
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DNA binding;
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Pred. No. 6.90e-01;
3; Mismatches 1
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                                      ##cross-references FlyBase:FBgn0001075
CLASSIFICATION #superfamily cadherin-related tumor
repeat homology; EgF homology
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Best Local Similarity 42.9%;
Matches 6; Conservative
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#title
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Bryant, P.J.; Goodman, C.S.
#journal Cell (1991) 67:853-868
#title The fat tumor suppressor gene in Drosophila
#title member of the cadherin gene superfamily.
#cross-references MUID:92069752
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##molecule_type DNA
##residues 1-1264 ##label ESW
##cross-references EMBL:X92670
##cross-references EMBL:X92670
##note the nucleotide sequence
##note Library, October 1995
                                                                                                               **residues 143-485;1279-5147 ##label ##cross-references GB:M80537
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MIPS:YGL133v
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Escribano, V.
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(Drosophila melanogaster)

#formal_name Drosophila melanogaster
30-Sep-1993 #sequence_revision 30-Sep-1993 #+~
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#length 1264 #molecular-weight 145642 #checksum 9929
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Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hıckey, E.K.; Gwinn, M.; Dougherty, B.; Tomb. J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.; Bowman, C.; Gazland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.; Smith, H.O.; Venter, J.C.
                                                                                                                                                                                                                                                F70126 #type complete translation elongation factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##experimental_source strain B31
CLASSIFICATION #superfamily translation elongation factor EF-P
SUMMARY #length 192 #molecular-weight 21413 #checksum
                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.3%;
Best Local Similarity 45.5%;
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Best Local Similarity 53.3%;
Matches 8; Conservative
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                                                                                                                       #journal #title
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#journal
#title
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#title
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#cross-references MUID:98065943
#accession F70126
                                                               #cross-references MUID:90360979
#accession S11693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type DNA
##residues 1-192 ##label KLE
##cross-references GB:AE001132; GB:AE000783; NID:g2688107;
##cross-references GB:AAC66610.1; PID:g2688116; TIGR:BB0214
##molecule_type mRNA
##residues 1-877 ##label LIA
##cross-references EMBL:X53615; NID:g164; PIDN:CAA37677.1; PID:g664894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues 1-108 ##label HES
##cross-references EMBL:AJ222776; NID:el203983; PID:el203984
##experimental_source cv. Haisa, leaf
##experimental_source cv. Haisa, leaf
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                                                                                                 EMBO J. (1990) 9:2701-2708 Identification and cloning of two bovine endothelial cells.
                                                                                                                                                                                                S11693
S11693
                                                                                                                                                                                                                                    % **Cadherin precursor - bovine (fragment)
#formal_name Bos primigenius taurus #common_name cattle
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hess, W.R.; Golz, R.R.; Boerner, T.
Plant Sci. (1998) 133:191-201
Analysis of randomly selcelted cDNAs reveals the expression of stress and defence related genes in the barley mutant alostrians.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #formai_name Hordeum vulgare #common_name barley
30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change
30-Apr-1999
                                                                                                                                                                            Liaw, C.W.; Cannon, C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T05921 *type fragment N-carbamyl-L-amino acid amidohydrolase homolog -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature (1997) 390:580-586 Genomic sequence of a Lym
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 7.00e+00;
5; Mismatches 1
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Pred. No. 4.45e+00;
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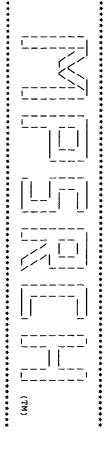
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FEATURE
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                                                                                                         Query Match 56.3%;
Best Local Similarity 40.0%;
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161,244,296,373,
543,593,622,663
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356-468
471-576
577-685
686-717
718-877
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131-685
                                       271 LNGMLRYRILSOAPS 285
1 LNSKIAFKIVSQEPA 15
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TION *superfamily cadherin; cadherin repeat homology calcium binding; cell adhesion; duplication; glycoprotein;
                                                                                                                                                                     pred:
#length 877
                                                                                      Conservative
                                                                                                                                                                                                                                                            #product N-cadherin *status predicted *label MAT\
#domain extracellular *status predicted *label EXT\
#domain cadherin repeat homology *label CR1\
#region cadherin binding *status predicted\
#domain cadherin repeat homology *label CR2\
#domain cadherin repeat homology *label CR3\
#domain cadherin repeat homology *label CR4\
#domain cadherin repeat homology *label CR4\
#domain cadherin repeat homology *label CR5\
#domain cadherin repeat homology *label CR5\
#domain transmembrane *status predicted *label INT\
#region serine-rich\
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                                                                                                                                                                            *checksum 8685
                                                                                                         Score 54; DB 1; I
Pred. No. 7.00e+00;
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Search completed: Sat May 13 07:10:30 Job time : 9 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 07:05:41 2000; MasPar time 79.42 Seconds 5.752 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-991-628-3 (1-15) from US08991628.pep 96 1 LNSKIAFKIVSQEPA 15

Scoring table:

PAM 150 Gap 15

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 26.327; Variance 28.416; scale 0.926

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	v	4	w	N	1	NO.	Result
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54.2	55.2										56.3		59.4			62.5			90.6	90.6	100.0	Match	Query
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HOLLIDAY JUNCTION DNA	TA	BETA	BETA	ທ		RNA POLYMERASE BETA SU	ASK10 PROTEIN.	$^{\circ}$		EPITHELIAL-CADHERIN PR	REC	20	TED TU	HYPOTHETICAL 145.6 KD	7.	NEURAL-CADHERIN PRECUR	EPITHELIAL-CADHERIN PR	DESMOGLEIN 2 PRECURSOR	DESMOGLEIN 1 PRECURSOR	DESMOGLEIN 1 PRECURSOR	DESMOGLEIN 3 PRECURSOR	Description	
4.88e+00 4.88e+00	2.97e+00	2.97e+00		•	2.97e+00	1.79e+00	1.79e+00	•	٠	1.79e+00	•	•	. 79e	.79e-		7.53e-02	. 53e	. 24e	5.08e-09	•	. 17	Pred. No.	

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ALIGNMENTS

K R R R R R R	88888888	888888888	3CCCCCCCCC	RESULT DD DD DD DD DD DD DD DD DD DD DD DD DD
EMBL; M76482; AAA60230.1; PIR; A41088; IJHIG3. HSSP; P09803; IEDH. MIM; 169615; PROSITE; PS00232; CADHERIN; 3. PFAM; PF00028; cadherin; 4. Cell adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein;	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	(POTENTIAL): (P	UENCE FROM N.A. JAMES 192669753. gai M., Klaus-Koytun V., Stanley J.R. gai M., Klaus-Koytun V., Stanley J.R. gaintibodies against a novel epitheli garis, a disease of cell adhesion."; 167:869-877(1991). FUNCTION: COMPONENT OF INTERCELLULAN INVOLVED IN THE INTERACTION OF PLACE FILAMENTS MEDIATING CELL-CELL ADHES: SUBCELLULAR LOCATION: TYPE I MEMBRAI TISSUE SPECIFICITY: EPIDERMIS, TONGI CARCINOMAS.	DSG3_HMMAN STANDARD; PRT; 999 AA. P32926; P32926; O1-OCT-1993 (Rel. 27, Created) O1-OCT-1997 (Rel. 27, Last sequence update) O1-NOV-1997 (Rel. 37, Last annotation update) DESMOGLEIN 3 PRECURSOR (130 KD PEMPHIGUS VULGARIS ANTIGEN) (PVA). DSG3. BUTHORO Sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Calcium-binding;

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Q03763;
01-0CT-1993 (Rel. 27, Cr
01-0CT-1993 (Rel. 27, La
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DESMOGLEIN 1 PRECURSOR (
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SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
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Koch P.J., "AR-1991) to the
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GOODWIN L., HILL J.E., Raynor K., Raszi L., Manabe Desmoglein shows extensive homology to the cadheri adhesion molecules.";
Biochem. Biophys. Res. Commun. 173:1224-1230(1990).
-- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME INVOLVED IN THE INTERCETLOUGH PROTEINS FILAMENTS MEDIATING CELL-CELL ADHESION.
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CHAIN
                                                   SEQUENCE OF 44-493 FROM MEDLINE; 91097553.
                                                                                      "Complete amino acid sequence of the epidermal polypeptide and identification of a second typology, J. Cell Biol. 55:200-208(1991).
                                                                                                                                                                      glycoprotein, as a
molecules.";
                                                                                                                                                                               Zimbelmann R., Franke W.W.;
"Identification of desmoqlein - -
                                                                                                                                                                                                                                                                                                  Dos. taurus (Bovine).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
Eukaryota; Metazoa; Ruminantia; i
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POTENTIAL.

DESMOGLEIN 3.

EXTRACELLULAR (POTENTIAL)

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

CADHERIN 1.

CADHERIN 2.

CADHERIN 3.

CADHERIN 3.

CADHERIN 3.

CADHERIN 3.

CADHERIN 4.

DESMOGLEIN REPEAT 1.

DESMOGLEIN REPEAT 2.

POTENTIAL.
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Matches 1
SEQUENCE FROM N.A.
TISSUE-KERATINOCYTES;
MEDLINE; 91271279.
Wheeler G.N., Parker A.E.,
Arnemann J., Rutman A.J., P
Buxton R.S., Magee A.I.;
"Desmosomal glycoprotein DG
                                                                                                                                                                                                                                           Q02413;
01-OCT-1993
01-OCT-1993
01-NOV-1997
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CONFLICT
SEQUENCE
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EMBL; X57784; CAA40930.1; -.
EMBL; M58165; AAA62709.1; -.
PIR; S14603; IJBOG1.
HSSP; P09803; IEDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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-!- TISSUE SPECIFICITY: EPIDERWIS, MUZZLE, TONGUE AND
-!- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE (POTENTIAL).
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Cell adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein;
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(Rel. 27, Last sequence update)
(Rel. 35, Last annotation update)
1 PRECURSOR (DESMOSOMAL GLYCOPROTEIN
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Pidsley
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CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
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DESMOGLEIN 1.
EXTRACELLULAR
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WW; ADE46133F8B77C11
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ses D.A.,
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Matches 1
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Q14126;
Q1-NOV-1997
Q1-NOV-1997
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SEQUENCE
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Eukaryota; Metazoa;
Eutheria; Primates;
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PIR: S16906: IJHUG1.
HSSP; P09803: 1EDH.
MIM: 125670: -
PROSITE: PS00232: CADHERIN:
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Cell adhesion; Signal; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EPIDEMMIS, TONGUE, TONSILAND E
DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
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SIMILARITY: BELONGS
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Similarity 80.0%;
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2 PRECURSOR
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CYTOPLASMIC (POTENTIAL).

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CADHERIN 2.

CADHERIN 3.

CADHERIN 3.

CADHERIN 4.

DESMOGLEIN REPEAT 1.

DESMOGLEIN REPEAT 3.

DESMOGLEIN REPEAT 5.

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AND INTERMEDIATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene. Eur. J. Cell Biol. 55:200-208(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00028; cadherin; 4. Cell adhesion; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIAT FILAMENTS MEDIATING CELL-CELL ADHESION.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-!- TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND CARCINOMAS.
-!- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
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SIGNAL
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                                                                                   191 LNSKISYRIVSLEPA
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JIOI 55:200-208(1991).
COMPONENT OF INTERCELLULAR DESMOSOME
COMPONENT OF PLAQUE PROTEINS
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DESMOGLEIN REPEAT 3.
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POTENTIAL.
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CYTOPLASMIC
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CADHERIN 4.
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EXTRACELLULAR (POTENTIAL):
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CAD1_MOUSE (P09803; Q61377; 01-MAR-1989 (Re:

(Rel. 10, Created)

STANDARD;

884 ₹

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MEDLINE: 96271285.

Overduin M., Tong K.I., Kay C.M., Ikura M.;

Overduin M., Tong K.I., Kay C.M., Ikura M.;

"1H, 15N and 13C resonance assignments and monomeric structure of the amino-terminal extracellular domain of epithelial cadherin.";

J. Blomol. NNR 7:173-189(1996).

-i- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS. THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extrement between Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsendan.email to licenseeisb-sib.ch).
EMBL; X06115; CAA29488.1; -. EMBL; X60961; CAA43292.1; -. EMBL; X60962; CAA43292.1; JO
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eurheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
EPITHELIAL-CADHERIN PRECURSOR (E-CADHERIN) (UVOMORULIN) (ARC-1).
                                                                                                                                                                                                                                                                                                                                                                                                   "Structural basis of calimerization.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Behrens J., Loewrick O., Klein-Hitpass L., Birchmeier W.;
"The E-cadherin promoter: functional analysis of a G.C-rich reg
and an epithelial cell-specific palindromic regulatory element.
Proc. Natl. Acad. Sci. U.S.A. 88:11495-11499(1991).
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Ringwald M., Schuh R., Vestweber D.,
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Nature 329:341-343(1987).
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                                                                                                                                                                    SORTING OF HETEROGENEOUS CELL TYPES.
SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: NON-NEURAL EPITHELIAL TISSUES.
SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
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) J. 6:3647-3653(1987).
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01-NOV-1990 (Rel. 16, Created)
01-OCT-1996 (Rel. 34, Last sequence updat
01-NOV-1997 (Rel. 35, Last annotation upc
NEURAL-CADHERIN PRECURSOR (N-CADHERIN).
CDH2 OR CDHN OR NCAD.
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                                                                      SEQUENCE FROM N.A. MEDLINE; 91016946. Reid R.A., Hemperly : "Human N-cadherin: no
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Reid R.A.;
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PROSITE: PS00232; CADHERIN; 5.
PFAM; PF00028; cadherin; 5.
PFAM; PF01049; Cadherin_C_term; 1.
Cell adhesion; Glycoprotein; Phosphorylation; Transmembrane; Cell adhesion; Glycoprotein; Phosphorylation; Transmembrane; Calcium-binding; Repeat; Signal; 3D-structure.
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Res. 18:5896-5896(1990)
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-> F (IN REF. 2).
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(NOV-1990)

to the EMBL/GenBank/DDBJ databases

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WEDLINE; 9034/402.

WEDLINE; 9034/402.

Walsh F.S., Barton C.H., Putt W., Spurr N., Goodfellow P.N.;

"N-cadherin gene maps to human clamber of the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second s
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EMBL; X54315; CAA88213.1; -.
EMBL; X542303; AAB22854.1; -.
EMBL; M34064; AAA02336.1; -.
EMBL; Z27420; CAA81799.1; -.
PIR; A38870; IJHUCN.
HSSP, P15116; INCH.
MIM; 114020; -.
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SEQUENCE FROM N.A.
SEDLINE; 92363956.
MEDLINE; 92363956.
Salomon D., Ayalon O., Patel-King R., Hynes 'Extrajunctional distribution of N-cadherin endothelial cells ";
" Call Sci. 102:7-17(1992).
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PFAM; PF01049; Cadherin_C_term; 1.
Cell adhesion; Glycoprotein; Phosphorylation; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0205; CADHERIN.
PROSITE; PS00232; CADHERIN;
PROM: PF00028; Cadherin; 5.
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EMBL; Z4659; CAA86628.1; -.
PIR; S33388; S33388
HSSP; P06601; IFJL.
SGD; L0002540; YOX1
PROSITE; PS00027; HOMEOBOX_1; 1
PROSITE; PS50071; HOMEOBOX_2; 1
PFAM; PF00046; homeobox; 1.
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P34161;
O1-FEB-1994 (Rel. 28, C:
O1-OCT-1996 (Rel. 34, La
O1-OCT-1996 (Rel. 34, La
HOMEOBOX PROTEIN YOX1.
YOX1 OR YMLO27W.
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                                                                                                                                                                           SEQUENCE
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Badcock K., Churcher C., Barrell B.G., Rajandream M.A.,
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: IN VITRO, IS CAPABLE OF BINDING TO THE DNJ
LEUCINE TRNA GENE.
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                                                                                                                                                                                                                                       Homeobox; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homeobox gene.";
Chromosoma 102:174-179(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                      364 KFGFKIVDQQP 374
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llarity 63.6%;
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YGN3_YEAST STANDARD; PRT; 1264 AA.

P53125;
T 01-CCT-1996 (Rel. 34, Created)
T 01-CCT-1998 (Rel. 34, Last sequence update)
T 15-DEC-1998 (Rel. 37, Last annotation update)
E HYPOTHETICAL 145.6 KD PROTEIN IN RPLIB-CEG1 INTERG:
SN YGL133W OR G2842.

OS Saccharomyces cerevisiae (Baker's yeast).
OS Saccharomyces cerevisiae (Baker's yeast).
CE Sukaryota: Fung1: Ascomycota: Saccharomycetes: Saccharomycetes: Saccharomycetes: Saccharomycetes: Saccharomycetes: Saccharomycetes: Saccharomycetes: Saccharomycetes: Saccharomycetes:
    RP SEQUENCE FROM N.A.

RA MEDLINE, 92069752.

RA MAHONEY P.A., Weber U., Onofrechuk P., Biessmann H., Bryant P.J.,

RA MAHONEY P.A., Weber U., Onofrechuk P., Biessmann H., Bryant P.J.,

RA Goodman C.S.;

RT "The fat tumor suppressor gene in Drosophila encodes a novel member

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Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAT_DROME STANDARD; PRT; 5147 AA. p33450; O1-FEB-1994 (Rel. 28, Created) O1-FEB-1996 (Rel. 33, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR)
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MEDLINE; 96437978.
ESCRIBANO V. Eraso P. Portillo F., Mazon M.J.;
"Sequence analysis of a 14.6 kb DNA fragment of serevisiae chromosome VII reveals SEC27, SSMLb, a cerevisiae chromosome VII reveals sec27, SSMLb, a cadenosylmethionine-dependent enzyme and six new frames."
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SEQUENCE 12
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Metazoa; Arth
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1264 AA; 145642
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PRINTS; PR00205; CADHERIN; 2
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PROSITE; PS00022; EGF_1; 4.
PROSITE; PS01186; EGF_2; 2.
PRAM; PF00008; EGF; 4.
PFAM; PF000028; cadherin; 34.
PFAM; PF00054; laminin_G; 2.
Cell adhesion; Signal; Transn
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laminin_G; 2.
Signal; Transmembrane; Cytoskeleton;
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  EGF-like domain.
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RX MEDLINE; 90360979.

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Liaw C.W., Cannon C., Power M.D., Kiboneka P.K., Rubin L.L.;

RA Liaw C.W., Cannon C., Power M.D., Kiboneka P.K., Rubin L.L.;

RA Hidentification and cloning of two species of cadherins in bovine

RT Identification and cloning of two species of cadherins in bovine

RT endothelial cells.";

CC ITENDO J. 9:2701-2708(1990).

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
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-I- FUNCTION: INVOLVED IN PEPTIDE BOND SYNTHESIS. STIMULATE EFFICIENT TRANSLATION AND PEPTIDE-BOND SYNTHESIS ON NATIVE OR RECONSTITUTED 70S RIBOSOMES IN VITRO. PROBABLY FUNCTIONS INDIRECTLY BY ALTERING THE AFFINITY OF THE RIBOSOME FOR AMINOACYL-TRNA, THUS INCREASING THEIR REACTIVITY AS ACCEPTORS FOR PEPTIDYL TRANSFERASE (BY SIMILARITY).
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P12830; Q14216;
Q1-OCT-1989 (Rel. 12, Created)
Q1-OUL-1993 (Rel. 26, Last sequence update)
Q1-UUL-1999 (Rel. 38, Last annotation update)
EPITHELIAL-CADHERIN PRECURSOR (E-CADHERIN) (UVOMORULIN)
CDH1 OR UVO OR CDHE.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Eukaryota; Primates; Catarrhini; Hominidae;
                 TISSUE=LIVER;
MEDLINE; 89031725.
Mansouri A., Spurr
                                                                                                                    SEQUENCE FROM N.A.
Kelker W., Warda A
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                                                                    SEQUENCE OF 172-311
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; PF01049; Cadherin_C_tes
adhesion; Glycoprotein;
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(XXX-1992)
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cloning
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                     Spurr N.,
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Pred. No.
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CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
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SER-RICH.
POTENTIAL.
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POTENTIAL.
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441B829ED871A249 CRC64;
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 P.N., Kemler localization
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DBJ databases
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Jpn. J
             MEDLINE; 98196671.
Guilford P., Hopkins J., Harraway, Harawira P., Taite H., Scoular R., "E-cadherin germline mutations in Nature 392:402-405(1998).
                                                                                                                                                                                                                                                                         Temura G., Santo K., Satodate n.,
Terashima M., Saito K., Satodate n.,
"Inactivation of the E-cacherin gene
"Inactivation of the E-cacherin gene
                                                                                                                                                 Soares P., Berx G., van Roy F., & "E-cadherin gene alterations are Int. J. Cancer 70:32-38(1997).
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Jpn. J. Cancer Res.
[8]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS GYNECOLOGIC CANCERS MEDLINE; 94355985. Risinger Ji., Berchuck A., K"Mutations of the E-cadherin Nat. Genet. 7:98-102(1994).
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[7]
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Becker K.-F., Atkinson M.J., Reich Siewert J.R., Hoefler H.; F-cadherin gene mutations provide
   Nature 392:40
                                                                                                               VARIANTS ASP-336 AND ILE-470
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MEDLINE; 97138061
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"E-cadherin gene mutations
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Berx G., Becker K.-F., Hoefler H.,

Berx G., becker K.-F., Hoefler H.,

Mutations of the human E-cadherin
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MEDLINE; 95049851
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MEDLINE; 94380041.
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lochem. Biophys. Res.
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Acad. Sci. U.S.
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91:1858-1862(1994).
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                             J., McLeod M., McLeod
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EMBL: Z18923: CAA79356.1: -.
EMBL: K12790: CAA31279.1: -.
EMBL: L34545: AAA21764.1: -.
PIR: S25141: IJHUCE.
PIR: S37654.
HSSP: P09803: 1SUH.
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                          VARIANT
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PFAM; PF01049; Cadherin_C_term; 1.

Cell adhesion; Glycoprotein; Phosphorylation; Transmembrane; Cell adhesion; Glycoprotein; Phosphorylation; Polymorph Calcium-binding; Repeat; Signal; Disease mutation; Polymorph
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SUBBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: NON-NEURAL EPITHELIAL TISSUES.
DISEASE: DEFECTS OF CDH1 IS REGARADED AS ONE OF THE MAIN MOLECULAR EVENTS INVOLVED IN DYSTUNCTION OF THE CELL-CELL ADHESION SYSTEM, TRIGGERING CANCER INVASION (GASTRIC, BREAST, OVARY, ENDOMETRIUM AND THYROLD) AND METASTASIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND THYROID) AND METASTASIS. SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
   473
                          470
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                                                                                               418
                                                                                                                                    400
                                                                                                                                                          370
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                                                                                                                                                                                                                                                       193
   473
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                                                                                                                                                                                                                                                      193
                                                                                                                                                                                                                                                                              154
882
707
731
731
882
262
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375
486
486
486
593
697
123
                                                                                                                                                                                                                                                                                                               POTENTIAL.

EPITHELIAL-CADHERIN.

EXTRACELLULAR (POTENTIAL).

CYTOPLASNIC (POTENTIAL).

CADHERIN 1.

CADHERIN 2.

CADHERIN 3.

CADHERIN 4.

CADHERIN 5.

SER-RICH.
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.
 /FTIG-VAR_001315.
7 -> L (IN DIFFUSE GASTRIC CANCER).
/FTIG-VAR_001316.
V -> N (IN DIFFUSE GASTRIC CANCER).
                                                                                           HETEROZYGOSITY).
/FTId-VAR_001312.
MISSING (IN GASTRIC CARCINOMA).
                                                                                                                                                                                          /FTId-VAR_001308.
N -> S (IN LOBULAR BREAST CARCINOMA)
/FTId-VAR_001309.
                                                                      /FTId-VAR_001313.
E -> Q (IN DIFFUSE
                                                                                                                                                                                                                                          /FTId=VAR_001306.
T -> P (IN DIFFUSE GASTRIC CANCER).
/FTId=VAR_001307.
                                                           /FTId-VAR_001314.
                                                                                                                                  MISSING (IN GASTRIC
                                                                                                                                                          /FTId-VAR_001310.
D -> A (IN DIFFUS
                                                                                                                                                                                                                              MISSING (IN GASTRIC ADENOCARCINOMA).
                                                                                                                                              /FTId-VAR_001311
                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                             -> Y (IN DIFFUSE GASTRIC CANCER).
                                                                                                                                                         DIFFUSE
GASTRIC CANCER)
                                                                       GASTRIC CANCER)
                                                                                                                                                         GASTRIC CANCER)
                                                                                                                                 CARCINOMA; LOSS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism
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XX MEDLINE; 92062581.

XX HETZDERIG F., Willdermuth V., Wedlich D.;

XX HETZDERIG F., Willdermuth V., Wedlich D.;

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Best Local
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P33152;
01-OCT-1993
                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                           EMBL; X78546; CAA55292.1;
EMBL; X63719; CAA45251.1;
PIR; S43065; S43065.
HSSP; P09803; 1SUH.
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SEQUENCE
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BLASTOMERE-CADHERIN PRECURSOR (B-CADHERIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      members
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Crania
Batrachia; Anura; Mesobatrachia; Pipo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Xenopus cadherins: the maternal members of the family."; Mech. Dev. 47:213-223(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muller H.A., Kuhl M.,
Hausen P., Wedlich D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 95151580.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543
882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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97456
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/FTId-VAR_001321.
S -> G /TN C...
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R -> Q (IN DIFFUSE GASTRIC CANCER).
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S -> F (IN REF. 2).
E427118043A13C67 CRC64;
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A -> T (IN THYROID CANCER).
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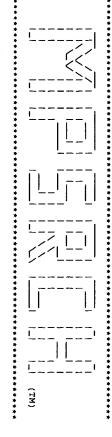
PRINTS; PR00205; CADHERIN

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                       cadherin.";
Neuron 20:1153-1163(1998)
                                                                                                            X-RAY CRYSTALLOGRAPHY (3.4 MEDLINE; 98318235.
Tamura K., Shan W.S., Hendr
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                                                                                                                                                                                                 "Structural basis of cell-cell adhesion Nature 374:327-337(1995).
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Gruebel G.,
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Matsunaga M., Hatta K., Ta
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Cell adhesion; Glycoprotein; Phosphorylation; Transmembrane;
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cadherin: role in
245:631-635(1989).
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01-FEB-1996 (Rel. 33, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
01-OCT-1996 (Rel. 34, Last annotation update)
ASK10 PROTEIN.
ASK10 OR YGR097W.
ASK10 OR YGR097W.
SACCharomyces cerevisiae (Baker's yeast).
Eukaryotts, Fungl. Ascomycotta; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomycetes; Saccharomyc
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the European Bioinformatics Institute. They
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See I
or send an email to license@isb-sib.ch).
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PFAM; PF01049; Cadherin_Cterm;
Cell adhesion; Glycoprotein; Phc
Calcium-binding; Repeat; Signal;
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
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Signal; 3D-structure.
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STRAIN-S288C / SEY6210;
MEDLINE: 97060018.
MEDLINE: 97060018.
Page N., Sheraton J., Brown J.L., Stewart R.S., Bussey H.;
"Identification of ASK10 as a multicopy activator of Skn7p-dependent transcription of a HIS3 reporter gene.";
Yeast 12:267-272(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: U27209; AAA67368.1; -. EMBL: Z72882; CAA97100.1; -. SGD: L0002770; ASK10.
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Hernandez K., Weber N., Wipfli P., Schmidheini T.;
Hernandez K., Weber N., Wipfli P., Schmidheini T.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PUTATIVE ACTIVATOR OF SKNT.
-!- SIMILARITY: TO YEAST YIL105C AND YNL047C.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Sat May 13 07:07:31 2000; MasPar time 140.71 Seconds 7.391 Million cell updates/sec

Run on:

Sequence: Description: Perfect Score: >US-08-991-628-3 (1-15) from US08991628.pep 96 1 LNSKIAFKIVSQEPA 15

Scoring table: PAM 150 Gap 15

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb112

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 25.549; Variance 30.093; scale 0.849

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

DE OJS902 PRELIMINARY: PRT; 993 AA. AC OJS902: DT 01-JAN-1998 (TIEMBLIEL 05, Created) DT 01-JAN-1998 (TIEMBLIEL 05, Created) DT 01-JAN-1998 (TIEMBLIEL 05, Last sequence update) DT 01-ON-1999 (TIEMBLIEL 12, Last annotation update) DE DESMOGLEIN 3 (FRAGMENT). CO EUKARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; CO EUKARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Murinae; Mus. RN 1503. CO EUKARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Mummalia; CO EUKARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Mus. RN 1503. CO EUKARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Mus. RN 1503. CO EUKARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Mus. RN 1503. CO EUKARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Mus. RN 1516; INCJ. RN 15
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Synechocystis sp. (Strain PCC 6803).
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core eudicots; R
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KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMTZU E., NAKAMURA Y., KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMOTO S., KIMURA T., MIYAJIMA N., HIOSONG A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA HOSONG II., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
Caenorhabditis elegans
Eukaryota; Metazoa; Ner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D90899; BAA166;
Hypothetical protein
SEQUENCE 138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis Sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."

DNA Res. 3:109-136(1996).
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"Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC004683; AAC28760.1;
SEQUENCE 1421 AA; 154325 MW; 1B6D2FF1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TABATA S.;
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN F.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C
elegans.":
                                                                                                                                                                                                                                                                                                                                       AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTIS Submitted (MAY-1998) to the EMBL/GenBank/DDBJ EMBL; AF063866; AAC97615.1; ... SEQUENCE 252 AA; 29068 MW; 3A7E442E CRC32;
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AFONSO C.L., TULMAN E.R., LI
"The genome of Melanoplus s.
J. Virol. 73:533-552(1999).
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01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
ORF MSV032 HYPOTHETICAL
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EMBL; 274033; CAA98472.1;
SEQUENCE 225 AA; 26356
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Similarity 53.3%;
8; Conservative
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SEQUENCE FILE
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TISSUE-BRAIN;
TISSUE-BRAIN;
X MEDLINE; 99087487.

RA NAGASE T., ISHIKAWA K., SUYAMA.
RA NAGASE T., ISHIKAWA K., OHARA O.;
RT "Prediction of the coding sequences of RT The complete sequences of 100 new cDNA RT for large proteins in vitro.";
RL DNA Res. 5:277-286(1998).

FMBL; AB018296; BAA34473.1;
FMBL; AB018296; BAA34473.1;
FMBL; AB018296; BAA34473.1;
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WARDLINE; 94150718.

MILSON R., ANDERSON K., BAYNES C., BERKS M.,

MILSON R., ANISCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,

AN ADNIFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

AN ACRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

AN ACKATON M., DEAR S., DU Z., DURBIN R., JILLIER L., JIER M., JOHNSTON L.,

AN ACKATON M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

AN ALIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

AN ARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

AN AND J., RECY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

AN AND J., RECY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

AN AND J., RECY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

AN AND J., RECY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

AN AND J., RECY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

AN AND J., RECY C., RIFKEN L., ROOPRA A., WAUTSON R.,

AN AND J., RECY C., RIFKEN L., ROOPRA A., SOUNDERS D., SHOWNKEEN R.,

AN AND J., RECY C., RIFKEN L., ROOPRA A., SOUNDERS D., SHOWNKEEN R.,

AN AND J., RECY C., RIFKEN L., ROOPRA A., WAUTSON R.,

AN AND J., RECY C., RIFKEN L., ROOPRA A., WAUTSON R.,

AN AND J., RECY C., RIFKEN L., ROOPRA A., WOHLDMAN P.;

THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

AN AND J., ROOPRA A., WOHLDMAN P.;

THE LEAST J., ROOPRA J., WOHLDMAN P.;

THE LEAST J., ROOPRA J., WOHLDMAN P.;

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THE LEAST J., ROOPRA J., ROOPRA J., WOHLDMAN P.;

THE LEAST J., ROOPRA J., ROOPRA J., ROOPRA J., ROOPRA J., ROOPRA J., ROOPRA J., ROOPRA J., ROOPRA J., ROOPRA J., ROOPRA J., ROOPRA J., ROOPRA J., ROOPRA J., ROOPRA J.
                                                                                                                                                                                                                                                                                                                 Query Match 57.3%;
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conser
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094853;
01-MAY-1999 (TrEMBLrel.
'01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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C36B1.11 PROTEIN.
C36B1.11.
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Eukaryota: Metazoa: Chordata:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIAA0753 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIAA0753.
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                                                                                                                                                               LNSKIAFKIVSQE
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KIAFKIVSQE
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    PRELIMINARY;
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Catarrhini; Hominidae;
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Pred. No. 3.62e+00
4; Mismatches
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Last sequence update)
Last annotation updat
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    PRT;
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No. 3.62e+00;
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    108
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RESULT 10
Q15855; Q16194; Q13799;
AC Q15855; Q16194; Q13799;
DT 01-NOV-1996 (TIEMBLIE1. 01
DT 01-NOV-1999 (TIEMBLIE1. 12
DE UYOMORULIN PRECURSOR (E-CA
GN UYO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chorda
OC Eutheria; Primates; Catarr
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Best Local
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Best Local
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055075; PRELIMINARY;
055075; PREMBLECL 06, C
01-UN-1998 (TREMBLECL 06, L
01-NOV-1999 (TREMBLECL 12, L
N-CADHERIN (FRAGMENT).
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01-JUN-1998;
01-JUN-1998;
01-AUG-1998;
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cricetilus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ALBOSTRIANS, CV. HAISA; TISSUE-WHITE LEAF;
HESS W.R., GOLZ R., BOERNER T.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ dat
EMBL; AJ222776; CAA10981.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TREMBLrel. 06, Created)
01-JUN-1998 (TREMBLrel. 06, Last sequence update)
01-JUN-1998 (TREMBLrel. 07, Last annotation update)
11-AUG-1998 (TREMBLrel. 07, Last annotation update)
11-AUG-1998 (TREMBLrel. 07, Last annotation update)
12-3 KD PROTEIN (FRAGMENT).
13-4 FRAGMENT (FRAGMENT)
14-4 FRAGMENT (FRAGMENT)
15-4 FRAGMENT (FRAGMENT)
15-4 FRAGMENT (FRAGMENT)
16-4 FRAGMENT (FRAGMENT)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-OVARY;
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238 /
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llarity 45.5%;
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26234 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.3%;
      Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
                                                                                                                                     el. 01, Last sequence update)
el. 12, Last annotation update)
(E-CADHERIN) (ARC-1/UVOMORULIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93
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12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOICHBERG P., GEIGER B.;
the EMBL/GenBank/DDBJ databases.
N: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
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Pred. No. 5.0
7; Mismatcl
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Pred. No. 5.
5; Mismatci
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Best Local Similarity
Matches 7; Conse
      Best Local
                              Query Match
                                                                              STRAIN-SPRAGUE-DAWLEY;

MEDLINE; 98187820.

CHUNG S.S., MO M.Y., SILVESTRINI B., LEE W.M.

"Rat testicular N-cadherin: its complementar;
cloning and regulation.";
Endocrinology 139:1853-1852(1998).

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROBLE; AF097593; AAC83818.1;
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROBLE; AF097593; AAC83818.1;
-1 FROSITE; PS00232; CADHERIN; 3.

PROSITE; PS00232; CADHERIN; 3.

Cell adhesion; Glycoprotein; Transmembrane; Geliadhesion; Glycoprotein; GC52E299 CRC3;
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9721Y3; PRELIMINARY;
0921Y3;
01-MAY-1999 (TIEMBLIEL 1
01-MAY-1999 (TIEMBLIEL 1
01-NOV-1999 (TIEMBLIEL 1
01-NOV-1999 (TIEMBLIEL 1
TESTICULAR N-CADHERIN.
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EMBL; 872391; AAD14
EMBL; 872491; AAD45
EMBL; L08599; AAA66
EMBL; X52279; CAA38
HSSP; P9803; ISUN
PROSITE; P$00232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Ve:
Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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BECKER K.F., ATKINSON M.J., REICH U.,
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RIMM D.L., MORROW J.S.;
"Molecular cloning of hur
the cadherin superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem.
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in; Transmembrane; Cal-
mw; 6C52E299 CRC32;
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Pred. No. 5.86e+00;
4; Mismatches 2
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ae; Murinae;
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"The complete nucleotide sequence of two cold-adapted, temperature-
sensitive attenuated mutant vaccine viruses (cpl2 and cp45) derived
from the JS strain of human parainfluenza virus type 3 (PIV3).";
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J. Vet. Med. Sci. 60:919-922(1998).
EMBL; AB012132; BAA32575.1; -.
PFAM; PF00946; Paramyx_RNA_pol; 1.
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Query Match 55.2%;
Best Local Similarity 46.7%;
Matches 7; Conservative
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Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                           MEICHTRY J., AMMRHEIN N., SCHALLER A.;

"The gene family of subtlisin-like proteases in Submitted (MAY-1998) to the EMBL/GenBank/DDBJ dane EMBL; x98930; CAA67430.1; -.

EMBL; x98930; CAA67430.1; -.

EMBL; AJ006379; CAA07000.1; -.

HSSP; 099405; IMPT.

MENDEL; 8813; Lyces;1086;8813.

PFAMM; PF00082; Peptidase_S8; 3.

PFINTS; PR00723; SUBTILISIN.

Protease; Serine protease.

SEQUENCE 775 AA; 83115 MW; ZEBF3C5E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 33.3%; Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 15
PRELIMINARY: PRT; 775 AA.
P93205.
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SERINE PROTEASE, SBT2.
SBT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISHIKAWA K., NAGASE T., NAKAJIMA D., SEKI N., OHIRA M., TANAKA A., KOTANI H., NOMURA N., OHARA O.; SUBMILTER (CCT-1997) to the EMBL/GenBank/DDBJ databases EMBL; AB007869; BAA23705.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 14
043159 PRELIMINARY; PRT; 464 AA.
043159;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. VFW8;
MEICHTRY J., AMRHEIN N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SCHALLER A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIAA0409 (FRAGMENT).
KIAA0409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Solanum.
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3 SKIAFKIVSQE 13
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Score 53; DB 10; Le
Pred. No. 9.43e+00;
5; Mismatches 3;
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Pred. No. 9.43e+00;
4; Mismatches 1
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7; Mismatches 3;
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databases.
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                                                                             Length 775;
    Indels
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Db 734 LSYKVTFKTVSRQKA 748 |: |::|| ||::| | Oy | 1 LNSKIAFKIVSQEPA 15

Search completed: Sat May 13 07:10:03 2000 Job time : 152 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Sat May 13 07:16:39 2000; MasPar time 3.02 Seconds 117.602 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-991-628-4 (1-15) from US08991628.pep 108 1 TPMFLLSRNTGEVRT 15

Scoring table: PAM 150 Gap 15

Searched: 188963 segs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 19.380; Variance 58.525; scale 0.331

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description	Pred. No.
: ب	108	100.0	15	⊢ ;	W04844	Self epitope of desmog	6.82e-05
2	108	100.0	15	Ь	81	oglein-3 206	.82e-0
w	108	100.0	15	L	W78815	3 protein	2e-
4	108		614	_	0	vul	.82e-
ហ	108	•	999	\vdash	R30742	phiqus vu	_
6	88	٠	778	_	œ	Pemphigus foliaceus an	
7	61	56.5	583	μ	R07999	Asparagine synthetase	:
œ	61		586	<u>_</u>	R07998		
9	60		163	ب	W38654	-	
10	59		919	ب	R86867		
11	57		263	L	W13010	Segment of desmosomal	
12	57	٠	560	μ	W13009	of.	
13	55	-	660	۳	R69633		8.73e+01
14	55		662	۳	R69632		•
15	55	•	662	Ь	W12772	Human interleukin-12 b	•
16	54	•	325	\vdash	W92443	Mouse MC5 protein.	•
17	54	•	325	ب	W87870	Mouse melanocortin rec	•
18	54	•	325	ب	W79688	ept	٠
19	54	•	325	٢	W19705	Melanocortin-5 recepto	1.11e+02
20	54	٠	325	۳	W33725	Mouse melanocortin-5 (•
21	54	•	325	-	R79501	မ	•
22	54	•	325	سر	W41067	Mouse melanocortin-5 r	1.11e+02
23	54	50.0	325	_	W37833	Mouse melanocortin-5 r	•

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Query Match 100.0%; Best Local Similarity 100.0%; Matches 15; Conservative

Score 108; DB 1; Length 15; Pred. No. 6.82e-05; 0; Mismatches 0; Indels

0;

Gaps

0;

45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30	29	28	27	26	25	24
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46.3	46.3	46.3	46.3				46.3	46.3	46.3	47.2	47.2	47.2	47.2	49.1	50.0	•				50.0	50.0
928	916	878	720	472	297	297	225	193	166	1726	1686	552	400	609	746	746	809	809	555	555	433
ь	<u>بــر</u>	↦	<u>بــ</u>	μ.	_	μ.	L	₽.	Ľ	Ļ	<u>.</u>	ш	H	\vdash	_	ب	ب	_	ب	ш	-
W21017	Y10967	R85487	W19266	W40072	W92440	W87867	P70061	P80877	P70358	W38756	W70991	R24017	R10919	P30206	W84156	W85135	W84155	W85134	W84154	W85133	W00365
н. ру	Ξ. Ό	Hum	Lac	Hun	HE	BO	Se	Hook	Sec	rg dq	Hu	F	Hu	Se	HE	₽	Hu	₽	Hu	≥	Human
pylori cytoplasmic	pylori ORF hp5e1521	Human E-cadherin precu	Lactobacillus amylovor	Human retinoid recepto	Human MC2 protein.	Bovine melanocortin re		region #8 contg	Sequence encoded by pl	Phosphatidyl inositol	Human class II P13 kin	Fusion protein GM-CSFR	Humam GM-CSF receptor.		Human desaturase enzym	A desaturase enzyme en	Human desaturase enzym	A desaturase enzyme en	Human desaturase enzym	A desaturase enzyme en	man cyclin Bl.

ALIGNMENTS

RESULT

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derived from the human desmoglein protein are described in W04841-47. Sequence 15 AA;	T-cells in individuals with the autoimmune disease. This peptide is derived from the human desmoglein 3 protein (amino acids 206-220)	protein, such as HLA-DR, which is associated with a human autoimmune disease and which binds to the polypeptide to activate autoreactive	sequence corresponding to a sequence motif for a MHC class II	polypeptide (whether self or non-self) includes an amino acid	e of	(MBP) polypeptide which is capable of tolerising an individual to an	either an isolated human non-collagen or non-myslin hasic protein	Claim 1; Page 40; 58pp; English.	•	identification of other self and non-self antigens implicated in	for	Pemphigus vulgaris auto-antigens and multiple sclerosis non-self	/42.	Strominger JL, Wucherpfennig KW;	(HARD) HARVARD COLLEGE	07-MAR-1995: 103-10796	07-WAR-1996. M03183	WO9627387-A1.	Homo sapiens.	influenza; haemagglutinin; reovirus; sigma protein.	human papillomavirus; Epstein-Barr virus; DNA polymerase;	herpes simplex virus: adenovirus: phosphomannomutase.	<pre>autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte; pemphiqus vulgaris; desmoglein; multiple sclerosis;</pre>	Tolerisation; self-epitope; antigen; autoimmune disease;	Self epitope of desmoglein 3, implicated in autoimmune disease.	18-FEB-1997 (first entry)	į	W04844 standard; peptide: 15 AA.

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RESULT ACCOUNT OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE OF THE PRINCE O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PT Microparticle encapsulated nucleic acids - for recombinant Microparticles encapsulated nucleic acids - for recombinant PT Microparticles (Column 4; 42pp; English.)

Disclosure; Column 4; 42pp; English.

CC The patent describes a new preparation of microparticles each comprising a polymeric matrix and a nucleic acid. The polymeric matrix consists of one or more synthetic polymers having a solubility CC and at least 90% of the microparticles have a diameter of less than 1 mg/l (e.g. poly-lactic-co-glycolic acid);

CC 100 microns. The microparticles are useful for the delivery of nucleic acid sto phagocytic cells. In one embodiment the microparticles are colless than 20 microns in diameter and the nucleic acid (preferably in CC closed circular form) includes an expression control sequence operatively linked to a coding sequence, where the expression product cof the coding sequence is a polypeptide having a length and a sequence componed in mammals. The present sequence, an antigenic portion of desmoglein 3, is an example of an MHC class I peptide which can be expressed by the nucleic acid. It is associated with pemphigus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 1
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US5783567-A.
21-JUL-1998.
22-JAN-1997; 787547.
22-JAN-1997; US-787547.
(PANG-) PANGAER PHARM INC.
(PANG-) PANGAER PHARM INC.
CUTIES JM, Hedley ML, Langer RS;
WPI: 98-427077/36.
                                                                                                                                                                                                                                                                                                                          Synthetic. W09831998-A1. W09831998-A1. 23-JUL-1998. U01499. 22-JAN-1998; US-003253. 22-JAN-1997; US-787547.
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W64816
W64816;
A microparticle preparation (MP) has been developed, consisting of microparticles having a diameter of less than 100 mu m. The MP comprises: (a) a polymeric matrix (PM) consisting of one or more synthetic polymers having a solubility in water of less that 1 mg/l; and (b) an expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 3
W78815
                                                                                                                             Disclosure; Page 8; 101pp;
                                                                                                                                                  gene therapy
                                                                                                                                                                                                                                           (PANG-) PANGAEA PHARM INC.
Curley JM, Hedley ML, Langer
WPI; 98-427556/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Desmoglein 3 protein fragment 206-220.

Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen; class II associated peptide; pathogen; gene therapy; genetic disease; infection; downregulation; immune response.
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17-NOV-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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Similarity 100.0%;
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Pred. No. 6.82e-05;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 15; Conservative
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30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T.
WPI; 96-388562/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fused protein recognised by pemphigus vulgaris auto:antibody - useful to treat and diagnose pemphis vulgaris Claim 1; Page 7-9; 9pp; Japanese. W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients with pemphis vulgaris resulting in autoimune disease. PV is a rare relapsing disease causing suprabasal, intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgGl hinge region and the resulting fusion protein is useful to treat or diagnose sequence 614 AA;
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W07908;
29-JAN-1997
                          14-JUN-1993 (first entry)
Human pemphigus vulgaris 130kD antigen.
Pemphigus vulgaris; skin disease; autoantibodies;
keratinocyte cell surface antigen; glycoprotein;
                                                                                                                                                      R30742 standard;
R30742;
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6.82e-05;
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                             cell adhesion
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Claim 1: Page 10-12: 17pp: Japanese.
This sequence represents a fused protein recognised by pemphigus
C foliaceus patient autoantibody which comprises the constant region
of IgG linked to the extracellular region of pemphigus foliaceus
antigen protein through the hinge portion. Pemphigus foliaceus
a chronic, generalised, vesicular and scaling skin eruption similar
to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion
protein is useful to treat pemphigus foliaceus. The antigen is
c especially administered through an adsorbent upon which the fusion
protein is immobilised via a carrier. The fusion protein is also
useful for detecting pemphigus foliaceus antibodies which is useful
in immondiagnosis. The fusion protein has little or no side effects.
Sequence 778 AA:
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Matches 1
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Best Local
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12-SEP-1995; JP-260899.
(NISH/) NISHIKAWA T.
WPI; 97-241758/22.
P-PSDB; T66428/
 R07999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M15489 standard; Protein; 778 AA.
W15489;
17-JUN-1997 (first entry)
18-pemphigus foliaceus antigen-IgG constant region fusion perministration foliaceus; autoantibody; constant region; IgG; extracellular region; antigen; hinge portion; skin; dermatitis herpetiformis; fusion protein; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding pemphigus vulgaris antigen - useful in proteins for diagnostic and therapeutic uses Disclosure; Fig 7; 50pp; English.

This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment of pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.

Sequence 999 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US7798918-A.
15-DEC-1992.
27-NOV-1991; 798918.
27-NOV-1991; US-798918.
(USSH) US DEPT HEALTH & HUMAN SERVICE.
AMBGGAL M. Klaus-Kovtun V, Stanley JR;
WPI; 93-067436/08.
                                                                                                                                                                                                                                                                                                                                                                                                         Pemphigus
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            standard;
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he hinge region used to treat pemphigus foliaceus
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llarity 66.7%;
Conservative
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            protein;
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Mismatches 0;
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1.76e-02
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W09013633-A.
15-NOV-1990.
02-MAY-1990;
03-MAY-1989;
26-APR-1990;
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Disclosure; Fig 2B; 91pp; English.
Disclosure; Fig 2B; 91pp; English.
The DNA sequence encoding this protein was isolated from cDNA clones selected from a pea nodule cDNA library from the "Sparkle" variety of P.sativum. Pea ASI cDNA was used as a probe.
The protein is produced by expression vectors containing the AS2 coding sequence. Recombinant AS can be used to engineer herbicide resistance, as a dominant selectable marker, to select novel herbicides or compounds useful for synchronising plant cells in
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15-NOV-1990.
02-MAY-1990;
03-MAY-1989;
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See also Q05598, Q06622 and Q06623.
                                                                                                                                                                                                               region
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Coruzzi GM, Tsai FY;
WPI; 90-361471/48.
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Pagaragine synthetase AS2.
Asparagine synthetase; transgenic plant; herbicide resistance; drought tolerance; nitrogen fixation; pea.
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U02443.
US-347302.
US-514816.
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; US-347302.
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/note= "conserved in human AS .
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Pred. No. 2.03e+01
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ALAMERA SOCOCOSOSOS
            PS. Claim 12: Page 407: 483pp; English.

CC This sequence represents a Streptococcus pneumoniae protein that, based con homology with an Escherichia coll protein, is a aspartate ammonia con homology with an Escherichia coll protein, is a aspartate ammoniae con homology with an Escherichia coll protein, is a aspartate ammoniae con homology with a sequence of the invention.

CC The DNA sequences were isolated from Streptococcus pneumoniae strain collops; (NCIMB 40794). The Streptococcus pneumoniae proteins of the collops; (NCIMB 40794). The Streptococcus pneumoniae proteins of the collops; (NCIMB 40794). The Streptococcus pneumoniae proteins can be used to induce an immunological response considering nucleic acids in a vector adequate to produce antibody con a mammal by inoculation with the S. pneumoniae proteins or delivery cof the encoding nucleic acids in a vector adequate to produce antibody conform the collops of inhibiting their bloactivity. In particular the proteins of companies can also be used to identify antimicrobial compounds which are companies can be used to prevent adhesion of bacteria to mammalian conformations of pathogenesis in infections initiated other than by the companies to protein of pathogenesis in infections initiated other than by the companies to the conformal techniques.
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Best Local s
Matches
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The DNA sequence encoding this protein was isolated from cDNA clones selected from a pea nodule cDNA library from the "Sparkle" variety of P.sativum. Human AS cDNA was used as a probe.

The protein is produced by expression vectors containing the ASI coding sequence. Recombinant AS can be used to engineer herbicide resistance, as a dominant selectable marker, to select novel herbicides or compounds useful for synchronising plant cells in
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Coruzzi GM, Tsai FY;
WPI; 90-361471/48.
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See also Q06599,
Sequence 586 AJ
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14-MAY-1996; US-017670
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7; Conservative
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EECHAM PLC.
Knowles DJC
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Pred. No. 2.03e+01;
2; Mismatches 0
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PS Claim 17; Page 130-132; 146pp; English.
CC R86865-R86867 represent the sequences for three protocadherins. This
CC R86865-R86867 represents the rat prococadherin pc5. These sequences are
CC related to cadherin, and possess cell adhesive ability. Cadherins are
CC glycosylated integral membrane proteins that are involved in cell-cell
CC adhesion. Cadherins are composed of an N-terminal extracellular domain
CC which consists of 5 unique subdomains, a membrane spanning domain, and a
CC cterminal cytoplasmic domain. The cytoplasmic domain interacts with the
CC cytoplasmic domain is not present in all cadherins, but in those
CC which possess it, it is essential for the cadherins adhesive function.
CC The cytoplasmic domain is not present in all cadherins, but in those
CC which possess it, it is essential for the cadherins adhesive function.
CC The cadherins which do not possess a cytoplasmic domain appear to
CC function via a different method from those with a cytoplasmic domain.
CC These sequences were isolated using primers 1 and 2 (see T03575 and
CC T03576) The proteins may have regulatory functions in the cell, as well
CC as the cell-cell adhesive properties. Antibodies produced against these
CC sequences are useful for modulating the binding activity of these
CC Sequences and can be used therapeutically.
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Best Local S
Matches
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Best Local Similarity 61.5%;
Matches 8; Conservative
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27-JUN-1994; US-268161.
(DOHE-) DOHENY EYE INST.
SUZUK1 S;
WPI; 96-068873/07.
                                                                                                                                                                                                                                                                                                                  21-NOV-1997 (first entry)
21-NOV-1997 (first entry)
Segment of desmosomal cadherin, desmoglein Dsg2.
Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithelial;
Carcinoma; desmosome; antibody; epitope; diagnosis; detection;
carcinoma; desmosome; antibody; epitope; diagnosis; detection;
23-AUG-1995; 031033.
23-AUG-1995; DE-031033.
(PROG) PROGEN BIOTECHNIK GMBH.
Franke WW, Schaefer S;
WPI; 97-146518/14.
                                                                                                                                                                                                                                                Homo sapiens.
DE19531033-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W13010 standard; W13010;
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Rattus rattus.
WO9600289-A1.
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1. No. 3.31e+01
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Franke ww, Schaefer S;

RMPI; 97-146518/14.

The present sequence is a segment of carcinoma micrometastases of epithelial or carcinoma cells, not bound to desmosomes, useful for diagnosis and treatment of carcinoma micrometastases of claim 7; Page 5; 8pp; German.

The present sequence is a segment of the desmosomal cadherin (DC), desmoglein Dsg2, which is exposed on the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab) directed against epitopes of the present sequence can be used to diagnose, i.e. to detect carcinoma cells, especially micrometastases, not bound to desmosomes to separate, enrich or detect living or fixed carcinoma cells by cell sorting methods and as a therapeutic to deliver agents, e.g. other Ab or toxins, to metastatic carcinoma, and detects parts of DC that are not accessible in desmosome bound cells, as in normal tissue or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody reactive with part of desmosomal cadherin - exposed on surface of epithelial or carcinoma cells, not bound to desmosomes, you useful for diagnosis and treatment of carcinoma micrometastases of Claim 9; Page 5; 8pp; German.

The present sequence is a segment of the desmosomal cadherin (DC), desmoglein Dsg2, which is exposed on the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab) directed against epitopes of the present sequence can be used to diagnose, i.e. to detect carcinoma cells, especially micrometastases, not bound to desmosomes, to separate, enrich or detect living or fixed carcinoma cells by cell sorting methods and as a therapeutic to deliver agents, e.g. other Ab or toxins, to metastatic carcinoma, and detects parts of DC that are not accessible in desmosome bound cells, as in normal tissue or
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DE19531033-A1.
27-FEB-1997.
23-AUG-1995; 031033.
23-AUG-1995; DE-031033.
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W13009;
21-NOV-1997
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Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithelial; carcinoma; desmosome; antibody; epitope; diagnosis; detection; micrometastasis; separation; enrichment; targetted delivery;
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                                                                                             pink encoding a low affinity interleukin-12 receptor - used to bind or scavenge IL-12 to cause immune suppression, e.g. to suppress graft-vs-host reaction, allograft rejection or inflammation, and to treat autoimmune conditions

Claim 4: Page 31-33; 6lpp: Engilsh.

A cDNA library of PHA-activated peripheral blood mononuclear cells in vector pEF-BOS was screened for interleukin-12 (IL-12) receptor CDNAs by panning. One isolated cDNA (QB3844) encoded a 662-amino acid low affinity IL-12 receptor (R69632). Another cDNA contained an additional 202 bp of 3'UTR; the deduced 660-amino acid sequence (R69633) showed an altered C-terminal sequence compared to R69632. Recombinant IL-12 receptor was expressed in COS cells, and can be sequence 660 AA;
                                                                                                                                                                                                                                                                      08-JUL-1994; 110657, 19-JUL-1993; US-094649, 19-JUL-1993; US-094713, 21-MAY-1994; US-248532, (HOFF) HOFFMANN LA ROCHE & Chizzonite RA, Chua AO, GWEI; 95-076349/11
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05-SEP-1995 (first entry)
Human interleukin-12 receptor:
Interleukin-12 receptor: II-12; immune suppression;
Immunosuppressive; graft-versus-host reaction; allograft rejection;
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inflammation; auto;
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352. .35
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(W222SKWS)"
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19-JUL-1993; US-094649.
19-JUL-1993; US-094713.
31-MAY-1994; US-248532.
(HOFF) HOFFMANN LA ROCHE &
Chizzonite RA, Chua AO, Gi
MPI; 95-076349/11.
                                                                                                                                                                      N-PSDB; 083844.

DNA encoding a low affinity interleukin-12 receptor - used to bind or scavenge IL-12 to cause immune suppression, e.g. to bind or scavenge IL-12 to cause immune suppression or inflammation, and to treat autoimmune conditions

Claim 4: Page 24-27; 61pp; English.

A cDNA library of PHA-activated peripheral blood mononuclear cells in vector PEF-BOS was screened for interleukin-12 (IL-12) receptor cDNA was sequenced (083844); it encoded a 662-amino acid low affinity IL-12 receptor (R69632); Recombinant IL-12 receptor was expressed in COS cells, and can be used for therapeutic or diagnostic purposes.

Sequence 662 AA;
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15-FEB-1995.
08-JUL-1994;
19-JUL-1993;
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R69632 standard; Protein;
R69632;
05-SEP-1995 (first entry)
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    HELLSRNTGEVET
                                              LFLLSRQGAACRT
                                                                                     h 50.9%;
Similarity 53.8%;
7; Conservative
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(W2225xWS)"
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e= "extracellular region"
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Pred. No. 8.73e+01;
2; Mismatches 4
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14 LFLLSRQGAACRT

7; Conser

Indels

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New interleukin-12 beta-2 receptor and high binding affinity complexes - have a high affinity for interleukin-12, and are used to treat autoimmune diseases

Sclaim 8: Page 37-41; S3pp; English.

Claim 8: Page 37-42; S3pp; English.

Claim 8: Page 37-42; S3pp; English.

Claim 8: Page 37-42; S3pp; English.

Claim 8: Page 37-42; S3pp; English.

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23-JUL-1996; 11807.
01-AUG-1995; US-001701.
30-MAY-1996; US-018674.
(HOFF) HOFFMANN LA ROCHE 6
Gubler UA, Presky DH;
WPI; 97-147515/14.
N-PSDB; T59732.
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W12772 standard; Protein;
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W12772; (first entry)
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llarity 53.8%;
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571
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329. .33
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352. .35
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/note= "cytokine receptor superfamily
(Cys52...Cys62SW)
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/note= "signal peptide cleavage
follows_Ala-23 ir Cys-24"
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/note= "cytokine_receptor superfamily
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Search completed: Sat May 13 07:16:47 2000 Job time : 8 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Sat May 13 07:16:14 2000; MasPar time 4.29 Seconds 165.096 Million cell updates/sec

Description: Perfect Score: Sequence: >US-08-991-628-4 (1-15) from US08991628.pep 108 1 TPMFLLSRNTGEVRT 15

Title:

Scoring table: PAM 150 Gap 15

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 27.219; Variance 35.537; scale 0.766

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222211111111 22222187654321 3210987654321	Result
8080 8080 8080 8080 8080 8080 8080 808	Score
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11049 1049 10443 1	Length
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H72278	A70755	A32992	JC2193	S16307	A71536	S36550	S17925	137892	YKMY	T02000	F70952	S04671	G70785	JW0071	D71089	B72582	S38673	A64100	AJECN	T06459	+00040
alpha-mannosidase-rel	hypothetical protein	cyclin Bl - human	melanocortin receptor	transcription activat	hypothetical protein	E6 protein - human pa	polynucleotide adenyl	IL12 receptor compone	citrate (si)-synthase	hypothetical protein	probable corA protein	₽.	hypothetical protein	asparagine synthase (hypothetical protein	probable nodulation A	desmoglein 2 - human	inner membrane copper		62K sucrose-binding p	COURT OPECATACLE PRODUCT
2.28e+01	2.28e+01	2.28e+01	2.28e+01	2.28e+01	2.28e+01	2.28e+01	1.50e+01	1.50e+01	1.50e+01	1.50e+01	1.50e+01	1.50e+01	1.50e+01	9.84e+00	9.84e+00	9.84e+00	6.42e+00		6.42e+00	6.42e+00	0.440

ALIGNMENTS

Ouery Match Best Local Simi Matches 15;	FEATURE 1-23 24-49 50-999 50-615 52-157 160-267 270-383 390-495 496-598 616-639 640-999 940-938 937-966 110,180,545	OR GE	RESULT 1 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS REFERENCE #authors #journal #title #toross-refere #accession
100.0%; Score 108; DB 1; Length 999; Similarity 100.0%; Pred. No. 1.65e-11; 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	#domain signal sequence #status predicted #label SIG\ #domain propeptide #status predicted #label PRO\ #product desmoglein homolog *status predicted #label MAT\ #domain extracellular #status predicted #label EXT\ #domain cadherin repeat homology #label CR1\ #domain cadherin repeat homology #label CR2\ #domain cadherin repeat homology #label CR3\ #domain cadherin repeat homology #label CR5\ #domain cadherin repeat homology #label CR5\ #domain cadherin repeat homology #label CR5\ #domain cadherin repeat homology #label CR5\ #domain transmembrane #status predicted #label INT\ #domain desmoglein repeat #label DG1\ #domain desmoglein repeat #label DG1\ #binding_site carbohydrate (Asn) (covalent) #status predicted #binding_site carbohydrate (Asn) (covalent) #status	##molecule_type mRNA ##rcsidues 1-999 ##label AMA ##cross-references GB:M76482; NID:g190751; PIDN:AAA60230.1; PID:g190752 CS GDB:DSG3 ##cross-references GDB:134030; OMIM:169615 ##cross-references GDB:134030; OMIM:169615 P_position 18q12.1-18q12.2 FICATION #superfamily cadherin; cadherin repeat homology FICATION #superfamily cadherin; dadhesion; duplication; glycoprotein; Calcium binding; cell adhesion; duplication; glycoprotein; Ctransmembrane protein	ILT 1 IJHUG3 #type complete E desmoglein 3 precursor - human RNATE_NAMES pemphigus vulgaris antigen #formal_name Homo sapiens #common_name man 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999 A41088 A41088 A41088 A41088 A41088 RENCE A41088 A41088 A41088 AH088

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**cross-references MUID:91271279
                                                                  24-49
50-1049
50-548
52-157
160-269
272-385
                                                                                                                                                                                                                                                                                                                                                                                                                                                        *authors Wheeler, G.N.; Buxton, R.S.; Parker, A.E.; Arnemann, Rees, D.A.; King, I.A.; Magee, A.I.

*journal Blochem. Soc. Trans. (1991) 19:1060-1064

*title Desmosomal glycoproteins I, II and III: novel members cadherin superfamily.

*cross-references MUID:92175187
                                                                                                                                                                                                                                                                                                                                                     #gene
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J. Cell Sci. (1991) 99:809-821

#title Structural analysis and expression of human
cadherin-like component of the desmosome.
**Cross-references MUID:92121251

#accession A61254
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                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
##residues 1-55 ##label WH3
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PNCE A39706
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##residues 1-1049 ##label BUX
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desmosomal glycoprotein I
#formal_name Homo sapiens #common_name man
30-Jun-1993 #sequence_revision 30-Jun-1993
22-Jun-1999
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submitted to the EMBL Data Library, November
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             #domain signal sequence #status predicted #label SIG\
#domain propeptide #status predicted #label PRO\
#product desmoglein #status predicted #label MAT\
#domain extracellular #status predicted #label EXT\
#domain cadherin repeat homology #label CRI\
#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR3\
#domain cadherin repeat homology #label CR4\
#region serine/threonine-rich\
#region serine/threonine-rich\
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          #journal
#title
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840-869
870-899
900-927
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*cross-references_MUID:92037656
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110,180
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                                                                                                                                                                                                                                                                                                               #authors Goodwin, L.; Hill, J.E.; Raynor, K.; Raszi, L.; Mane Cowin, P.

#journal Biochem. Blophys. Res. Commun. (1990) 173:1224-1230

#title Desmoglein shows extensive homology to the cadherin cell adhesion molecules.

#cross-references MUID:91097553

#accession A37785
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                                                                                                   ##residues 44-1043 ##label ZIM
##cross-references EMBL:X57784; NID:g436061; PIDN:CAA40930.1;
PID:g436062
                                                                                                                                           ##molecule_type mRNA
##residues 44-1
                                                                                                                                                                                                                                                      ##cross-references GB:M58165; NID:g162966;
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                                                                                                                                                                                                                                                                                          ##molecule_type mRNA
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#*residues 1-87;968-1043 ##label KO2
##cross-references GB:S64268; GB:S64270
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Koch, P.J.; Walsh, M.J.; Schmelz, M.; Zimbelmann, R.; Franke, W.W. Eur. J. Cell Biol. (1990) 53:1-12 Identification of desmoglein, a consti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Franke, W.W. submitted to the EMBL Data Library, March 1991
Complete sequence of the desmoglein precursor and evidence for the existence of different desmoglein genes expressed
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#domain desmoglein repeat #label DG1\
#domain desmoglein repeat #label DG2\
#domain desmoglein repeat #label DG3\
#domain desmoglein repeat #label DG4\
#domain desmoglein repeat #label DG4\
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#binding_site carbohydrate (Asn) (covalent)
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Pred. No. 1,37e-06;
5; Mismatches 0
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Best Local Similarity 60.0%;
Matches 9; Conservative
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                                                                                                                                                                                                      ##molecule_type DNA
                                                                                                                                                   ##residues 1-572 ##label DAN
##cross-references EMBL:248675; N:
PID:9747902
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                                       ##molecule_type DNA
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##residues 44-1001,'AQPPSAT'
##cross-references_GB:X57784
         #cross-references
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                                                              Fulton, L.
submitted to the EMBL Data Lit
                                                                                                                                                                                                                                              Dang, V.D.; Bolotin-Fukuhara, M.; Daignan-Fornier, B. submitted to the EMBL Data Library, March 1995 Multiple regulatory systems control expression of the Saccharomyces cerevisiae ASN1 and ASN2 genes at the transcription level.
                                                                                                                                                                                                                                                                                                                                                                               asparagine synthase (glutamine-hydrolyzing) (EC yeast (Saccharomyces cerevisiae) protein P9659.3; protein PR145w #formal_name Saccharomyces cerevisiae 19-May-1995 *sequence_revision 01-Sep-1995 *text 16-Jul-1999
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$52694
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calcium binding; cell adhesion;
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#domain cadherin repeat homology #label CR2\
#domain cadherin repeat homology #label CR2\
#domain cadherin repeat homology #label CR4\
#domain cadherin repeat homology #label CR4\
#domain transmembrane #status predicted #label TMM\
#domain intracellular #status predicted #label INT\
#domain desmoglein repeat #label DG1\
#domain desmoglein repeat #label DG3\
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                           1-572 ##label
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#domain propeptide #status predicted #label PRO\
#product desmeglein #status predicted #label MAT\
#product desmeglein #status predicted #label EXT\
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   572 ##label FUL
EMBL:U40829; NID:g1066476;
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Pred. No. 5.83e-05;
5; Mismatches 1
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duplication; glycoprotein;
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     PIDN: AAB68284.1;
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                           346 TPMFLLSRK 354
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##cross-references EMBL:X83099; N
PID:g642347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type DNA
                                                                                                                                                                                                                                                                                ##experimental_source strain
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Similarity 88.9%;
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Talla, E.; Nawrocki, A.; Del Bin
submitted to the Protein Sequence
S64433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   van Dyck, L.; Goffeau, A. submitted to the EMBL Data Library, December 1994 Submitted to the EMBL Data Library, December 1994 Genes for an asn synthase, a GLFG-motif nucleoporin and a putative homeobox-domain protein are identified on a 18.3 kb segment of the yeast chromosome VII also carrying MEP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asparagine synthase (glutamine-hydrolyzing)
- yeast (Saccharomyces cerevisiae)
protein G6358; protein YGR124w
#formal_name Saccharomyces cerevisiae
23 Aug-1995 #sequence_revision 19-Oct-1995 #
                                                                                                                                                                              #superfamily asparagine synthase (glutamine-hydrolyzing)
asparagine biosynthesis; ligase
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                                                                              Score 65; [
Pred. No. 1.
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Pred. No. 1.74e-01
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.; Del Bino, S.;
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.; Goffeau, A.
base, May 1996
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                                                                                                                                                                                      #authors Fong, S.T.; Camakaris, J.; Lee, B.T.
#journal Mol. Microbiol. (1995) 15:1127-1137
#title Molecular genetics of a chromosomal locus
tolerance in Escherichia coli K-12.
#cross-references MUID:95349397
#accession I41028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #journal Mol. Microbiol. (1993) 8:543-558
#title Nucleotide sequence of a 13.9kb segment of the 90kb virulence plasmid of Salmonella typhimurium: the presence of fimbrial biosynthetic genes.
#cross-references MUID:93316852
                                                                                                                                                                                                                                                                                                                                                                                     Analysis of the Escherichia coli genome VI: the region from 92.8 through 100 minutes. #cross-references MUID:95334362
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Best Local Similarity 80.0%;
#authors Crooke, H.; Cole, J.
#journal Mol. Microbiol. (1995) 15:1139-1150
#title The biogenesis of c-type cytochromes in Escherichia coli
requires a membrane-bound protein, DipZ, with a protein
disulphide isomarase-like domain.
#cross-references MUID:95349398
                                                                                                                                                                                                                                                                                             132 TLMFSLSR-TGEVRT 145
                                                                                                                    ##cross-references EMBL:236905; NID:g535290; PID:g581055
##note in this report, the codon GTG for Val-77
                                                                                                                                                    **residues
                                                                                                                                                                                                                                                                                                                                                            ##molecule_type DNA
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FICATION #superfamily Salmonella typhimurium hypothetical protein (peff 5' region)
## length 295 #molecular-weight 31162 #checksum 8332
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##residue
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##residues 'M',78-565 ##label RES
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19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change
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##experimental_source strain K-12, substrain MG1655

ERENCE
##authors Missiakes, D.: Schwager, F.: Raina, S.
#journal EMBO J. (1995) 14:3415-3424

#title Identification and characterization of a new di
#totle Somerase-like protein (DsbD) in Escherichia
#tross-references MUID:95354659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #journal Science (1997) 277:1453-1462
#title
The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
#accession F65223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
##residues 1-328,'V',330-565 ##label CRO
##cross-references EMBL:X77707
     ##residues
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##residues 462-540 ##label MIS
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##note in this report, the codon GTG for Val-77 was interpreted
as a start codon
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##residues 'M',
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Similarity 53.8%;
7; Conservative
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submitted to the EMBL Data Library, February 1994
The biogenesis of C-type cytochromes in Escherichia
requires an integral membrane protein with a prote
disulphide isomerase like domain.
                                                         Dietrich, F.S. submitted to the EMBL Data Library, December 1994. The sequence of S. cerevisiae cosmids 9537, 9581, and lambda clone 5898.
                                                                                                                                                                                                                                    #formal_name Saccharomyces cerevisiae
28-May-1993 #sequence_revision 24-Feb-1995 #text_change
21_Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dsbD; cycZ; CutA2; dipZ
inner membrane; redox-active disulfide; transmembrane
#length 565 #molecular-weight 61795 #checksum 2685
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Crooke,
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1-923 ##label DIE
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Pred. No. 4.41e-01;
3; Mismatches 3
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Indels

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#text_change

ir, P.;
; Weissenbach,
; C.;

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Best Local
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                                                                                             #title Dark-induced and organ-specific expression synthetase genes in Pisum sativum. #cross-references MUID:90151604
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                           ##cross-references EMBL:X52180; NID:g20651; PIDN:CAA36430.1;
                                                              ##molecule_type DNA
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Local Similarity 53.8%;
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#formal_name Pisum sativum #common_name garden pea
31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catalyzes ATP-dependent transfer of the amide group of glutamine to aspartate generating asparagine and glutamate asparagine biosynthesis synthase (glutamine-hydrolyzing) asparagine biosynthesis; ligase #length 581 #molecular-weight 65609 #checksum 7265
                                                                                                                                                Tsai, F.Y.; Coruzzi, G.M. EMBO J. (1990) 9:323-332
                                                                                                                                                                                   S11443
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11-Jun-1999 #sequence_revision 11-Jun-1999 #t
23-Jul-1999
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                                              1-583 ##label
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77.8%;
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pred. no. 1.10e+00;
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Pred. No. 4.41e-01;
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"">ucleic acid
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Similarity 77.8%;
7; Conservative
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                                 nces MUID: 96270368
S69182
                                                                Clarkson, D.T.
Plant Mol. Biol. (1996) 30:883-897
Molecular cloning and characterisation of asparagine synthetase from Lotus japonicus: dynamics of asparagine synthesis in N-sufficient conditions.
                                                                                                                                                                                                                                                                      S69182 #type complete
asparagine synthase (glutamine-hydrolyzing)
                                                                                                                                                                                                                    #formal_name Lotus japonicus
19-Mar-1997 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - Arabidopsis thaliana asparagine synthatase, glutamine-dependent; protein T2118.90 *formal_name Arabidopsis thaliana *common_name mouse-ear
                                                                                                                                       Waterhouse, R.N.;
Clarkson, D.T.
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th 583  #molecular-weight 65649  #checksum 2836
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77.8%;
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Pred. No.
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Pred. No. 1.10e+00;
2; Mismatches (
                    sequence not shown
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. 1.10e+00;
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*title Molecular cloning and characterisation of asparagine synthetase from Lotus japonicus: dynamics of aspara synthesis in N-sufficient conditions.

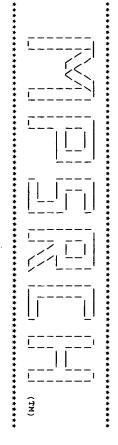
*cross-references MUID:96270368

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PID:g897773
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asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4)
garden pea
asparagine synthetase (glutamine-hydrolyzing)
#formal_name Pisum sativum #common_name garden pea
31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
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asparagine synthase (glutamine-hydrolyzing.
Lotus japonicus
#formal_name Lotus japonicus
19.Mar-1997 #sequence_revision 19-Mar-1997
16-Jul-1999
               Tsai, F.Y.; Coruzzi, G.M.
EMBO J. (1990) 9:323-332
Dark-Induced and organ-specific expression
synthetase genes in Pisum sativum.
nces MUID:90151604
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*accession T02978
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NT This protein is one of a family of glutamine amidotransferases that have dual specificity to utilize either glutamine or ammonia as a substrate. Two functional domains have been identified: an aminator domain, which catalyzes the ammonia dependent reaction, and a glutamine amide transfer domain, which binds glutamine and
                                                                                                   322 TPMFLMSRK 330
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PID:g984262

##experimental_source cultivar var.DEA; root meristem
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asparagine synthase (EC 6.3...) - maize
asparagine synthetase
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Metabolic regulation of asparagine synthetase gene expression in maize (Zeamays L.) root tips.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

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Title: >US-08-991-628-4
Description: (1-15) from US08991628.pep
Perfect Score: 108

Scoring table: PAM 150 Gap 15 Sequence:

TPMFLLSRNTGEVRT 15

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 27.727; Variance 32.559; scale 0.852

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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T "Desmosomal glycoprotein DGI, a component of functions, is related to the cadherin family molecules.";

Proc. Natl. Acad. Sci. U.S.A. 88:4796-4800/10-1-FUNCTION: COMPONEYM CT.
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DOMAIN 50
                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE; 91271279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; C
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                                                                                                                                                                                                                                                                                                                                       C. Natl. Acad. Sci. U.S.A. 88:4796-4800(1991).
FUNCTION: COMPONENT OF INTERCELLULAR DESMOSME JUNCTIONS.
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEL
FILAMENTS MEDIATING CELL-CELL ADHESION.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND ESOPHAGUS.
DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                           (POTENTIAL).
SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
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                                        125670;
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  PS00232; CADHERIN;
00028; cadherin; 4.
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Pred. No. 4.18e-13;
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CADHERIN 2.
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l; Hominidae; Homo.
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TISSUE-MUZZLE I
Koch P.J., Gold
Submitted (MAR
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01-OCT-1993
01-NOV-1997
SEQUENCE OF 44-493 FROM N.A.
MEDLINE; 91097553.
Goodwin L., Hill J.E., Raynor K., Raszi
"Desmoglein shows extensive homology to
adhesion molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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SEQUENCE
                                                    polypeptide and ide
                                                                                                                                     glycoprotein, as a member
molecules.";
                                                                                                                                                    Koch P.J., Walsh M.J., Schmelz Zimbelmann R., Franke W.W.; "Identification of desmoglein,
                                                                                                                                                                               SEQUENCE OF 44-1043 FROM TISSUE-MUZZLE EPITHELIUM; MEDLINE; 91168965.
                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
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Q03763;
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                                                    *Complete amino acid sequence of the epidermal desmoglein prec
polypeptide and identification of a second type of desmoglein
Eur. J. Cell Biol. 55:200~208(1991).
                                                                                                           REVISIONS,
                                                                                                                                                                                                                                                               Bovinae;
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Calcium-binding;
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                                                                                                                          Cell Biol. 53:1-12(1990).
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UZZLE EPITHELIUM;
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id (MAR-1991) to the E
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Last annotation updat
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        the
                                                                                      Zimbelmann
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       Manabe M., Cowir cadherin family
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SEQUENCE FROM
STRAIN-S288C ,
                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetaceae; Saccharomyces.
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EMBL; X57784; CAA40930.1; -.
EMBL; M58165; AAA62709.1; -.
PIR; S14603; IJBCG1.
HSSP; P09803; 1EDH.
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- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUN
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND
FILAMENTS MEDIATING CELL-CELL ADHESION.

- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
- TISSUE SPECIFICITY: EPPIDENMIS, MUZELE, TONGUE AND
- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
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Cell adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein;
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SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSONAL SUBFAMILY.
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Pred. No. 6.76e-06;
5; Mismatches 1
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W; ADE46133F8B77C11 CRC64;
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EXTRACELLULAR (POTENTIAL).
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"An 18.3 kb DNA fragment from yeast ch
unknown open reading frames, the gene
of Ty and three tRNA genes.";
yeast 13:171-176(1997).
[2]
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ASN1 YEAST STANDARD; PRT; 571 AA.
4501 YEAST STANDARD; PRT; 571 AA.
649089; 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] 1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE 1).
ASN1 OR YPR145W OR P9659.3.
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EMBL; Z72909; CAA97135.1; --
SGD; L0003156; ASN2
SGD; L0003156; ASN3
PROSITE; PS00443; GATASE_TYPE_
PFAM; PF00310; GATASE_2; 1
PFAM; PF00733; Asn_synthase; 1
                                                                                           Dang V.D., Valens M., Bolotin-Fukuhara M., Daignan-Fornier B. "Cloning of the ASN1 and ASN2 genes encoding asparagine synth in Saccharomyces cerevisiae: differential regulation by the CCAAT-box- binding factor.", Mol. Microbiol. 22:681-692(1996).
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ACT_SITE
SEQUENCE
     Johnston M., Andrews S Favello A., Fulton L., Hallsworth K., Hawkins
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Nawrocki A., del Bino S., Goffeau A.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE
PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.
-!- PATHWAY: ASPARAGINE BIOSYNTHESIS.
-!- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUT
                                                  SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 97109535.
                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetaceae; Saccharomyces.
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SIMILARITY: TO OTHER ASN SYNTHETASES.
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S., Brinkman R., Cooper J., Ding H., Du Z.
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ns J., Hillier L., Jier M., Johnson D.,
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Pred. No. 4.34e-02;
1; Mismatches (
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GATASE (BY SIMILARITY).
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EMBL: U40829; AAB68284.1; -...
SGD: L0002732; ASMI
PROSITE; PS00443; GATASE_TYPE_:
PFAM; PF00310; GATASE_2; 1.
PFAM; PF00733; ASM_Synthase; 1
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MEDLINE; 9534 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSBD_ECOLI STANDAKU,
P36655; P76796;
01-JUN-1994 (Rel. 29, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
THIOL.DISULFIDE INTERCHANGE PROTEIN DSBD (C-TYPE CYTOCHROME
BIOGENESIS PROTEIN CYCZ) (INNER MEMBRANE COPPER TOLERANCE PF
                                                                                                                                                                                                                                                                  Crooke H., Cole J.;
"The biogenesis of c-type cytochromes in membrane-bound protein, DipZ, with a prot isomerase-like domain.";
Mol. Microbiol. 15:1139-1150(1995).
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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

-:- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE
--- PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.

--- PATHWAY: ASPARAGINE BIOSYNTHESIS.
                                                                   "Molecular genetics of a chromosomal tolerance in Escherichia coli K-12.";
Mol. Microbiol. 15:1127-1137(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSBD OR CYCZ OR CUTA2 OR Escherichia coli. Bacteria; Proteobacteria;
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Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Ri
Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman
  SEQUENCE FROM N.A.
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CHARACTERIZATION.

MEDDINE; 95046265.

Sambongi Y., Ferguson S.J.;

Sambongi Y., Ferguson S.J.;

Sambongi Y., Ferguson S.J.;

"Specific thiol compounds complement deficiency in c-type propertion of the compounds complement deficiency in a membrane-bound disulphide isomerase-like protein.";

Leter 135:235-238 (1994).

C-!- FUNCTION: REQUIRED FOR DISULFIDE BOND FORMATION IN SOM PERIPLASMIC PROTEINS. ONE OF ITS FUNCTION COULD BE TO THE CYS RESIDUES IN APOCYTOCHROMES C IN A REDUCED STAT COVALENT LINKAGE WITH THE HEME.

C-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER COLLOWER STATES AND CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTR
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Burland V.D., Plun
Blattner F.R.;
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EMBL; U14003; AAA97035.1; ALT_INIT.
EMBL; AE000486; AAC77096.1; ALT_INIT.
EMBL; Z36905; CAA85375.1; -.
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Missiakas D., Hughes
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                                                                                                                                                         Sandersonia aurantiaca (Christmas-bells) (Chinese-lantern lily).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Liliales;
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Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Cherry Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry Chung E., Berno A., Brennan E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1944) to the EMBL/GenBank/DDBJ databases.
         TISSUE=TEPAL;
Eason J.R., K
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PFAM; PF00310; GATase_2; 1.
PFAM; PF00733; Asn_synthase; 1.
R PFAM; PF00733; Asn_synthase; 1.
Garase; Asparagine biosynthesis; Glutamine amidottume of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of 
P SEQUENCE OF 1-83 FROM N.A.

C STRAIN-CV: FELTHAM FIRST;
A Ngai N., Tsai F.Y., CORUZZI G.M.;
T Night 'Induced transcriptional repression of the pea AS1 gene
1 deptification of cis-elements and transfactors.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
C :- CATALYTIC ACTIVITY: ATP + L-ASPARRATE + L-GLUTAMINE - AMP
PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.
C :- PATHMAY: ASPARAGINE BIOSYNTHESIS.
C :- INDUCTION: DARK-INDUCED.
C :- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASN2_PEA STANDARD; PRT; 582 AA. P19252; 049926; 01-NOV-1990 (Rel. 16, Created) 01-FEB-1991 (Rel. 17, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) ASPARAGINE SYNTHETASE, ROOT [GLUTAMINE-HYDROLYZING] (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Dark-induced and organ-specific expression synthetase genes in Pisum sativum."; EMBO J. 9:323-332(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pisum sativum (Garden pea).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae;

Bukaryota; Pabaices; Pabaices; Pabaiceae; Papilionoidi

Core eudicots; Rosidae; eurosids I; Fabaices; Fabaceae; Papilionoidi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. SPARKLE; MEDLINE; 90151604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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CAPALYTIC ACTIVITY: ATP + L-ASPARTATE + L-G

PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.

PATHWAY: ASPARAGINE BIOSYNTHESIS.
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77.8%;
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Pred. No.
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3.25e-01;
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Best Local
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"Metabolic regulation of the gene encoding glutamine-dependent asparagine synthetase in Arabidopsis thaliana.";

Plant Physiol. 106:1347-1357(1994).

-i-CARALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE - AMP - PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.

-i-PARHWAY: ASPARAGINE BIOSYNTHESIS.

-i-SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMINE
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PPAM; PP00733; Asn_synthase; 1.

PPAM; PP00733; Asn_synthase; 1.

Ligase; Asparagine biosynthesis; Glutamine amidotransferase;

Ligase; Asparagine biosynthesis; Glutamine amidotransferase;

Multigene family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eddicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X52180; CAA36430.1; -. EMBL; Y13322; CAA73763.1; -. PIR; S11443; AJPMN2.
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Lam H.M., Peng S.
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Pred. No. 3.25e-01
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D (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                 Delavault P., Estabrook E., Albrecht H., Wrobel R., Yoder J.I.;
"Host root exudates increase gene expression of asparagine synthetase
in the roots of a hemiparasitic plant Triphysaria versicolor
(Scrophulariaceae).";
Gene 222:155-162(1998).
-I- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE - AMP +
PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.
-I- PATHWAY: ASPARAGINE BIOSYNTHESIS.
-I- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMINE
AMIDOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Triphysaria versicolor.
Triphysaria versicolor.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Asteridae; euasterids I; Lamiales; Scrophulariaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASNS_TRIVS STANDARD; PRT; 585 AA. 024661; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-FEB-2000 (Rel. 39, Last annotation update) ASPARAGINE SYNTHSTASE [GLUTAMINE-HYDROLYZING]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: L29083; AAA74359.1; -. HSSP; P17169; IGMS. PROSITE; PS00443; GATASE_TYPE_II; PFAM; PF00310; GATase_2; 1. PFAM; PF00733; Asn_synthase; 1.
                                                                                                                                           EMBL; AF014055; AAD05033.1; -.
EMBL; AF014055; AAD05034.1; -.
EMBL; AF014057; AAD05035.1; -.
EMBL; AF014057; AAD05035.1; -.
EMBL; AF014057; AAD05035.1; -.
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Score 61; DB 1;
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STANDARD; PRT; 585 AA.
P1925;
O1-WOV-1990 (Rel. 16, Created)
O1-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ASPARAGINE SYNTHETASE, NODULE [GLUTAMINE-HYDROLYZING]
(GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE).
ASSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HSSP; P17169; 1GMS.
PROSITE; PS00443; GATASE_TYPE_II; 1.
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ACT_SITE 1 1 GATASE (BY SIMILARITY).
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- CATALYTIC ACTIVITY: AND + L-ASPARTATE + L-GLUTAMINE - AMP PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.

-!- PATHWAY: ASPARAGINE BIOSYNTHESIS.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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Multigene family.
INIT_MET 0
ACT_SITE 1
                                                                                                                                                                        ASNS_MAIZE STANDARD: PRT; 585 AA. P49094; P49094; Ol-FEB-1996 (Rel. 33, Created) Ol-FEB-1996 (Rel. 33, Last sequence update) Ol-OCT-1996 (Rel. 34, Last annotation update) ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) DEPENDENT ASPARAGINE SYNTHETASE).
                      Zea mays (Maize).
Eukaryota; Viridiplantae;
euphyllophytes; Spermatoph
Poaceae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X52179; CAA36429.1; -.
EMBL; Y13321; CAA73762.1; -.
PIR; S11444; AJPMN1.
HSSP; P17169; IGMS.
PROSITE: PS00443; GATASE_TYPE_II;
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"Dark-induced and organ-specific expression
synthetase genes in Pisum Sativum.";
EMBO J. 9:323-332(1990).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;

core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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SIMILARITY: TO OTHER ASN SYNTHETASES.
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                                                             diplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biosynthesis; Glutamine
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3.25e-01
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Chevalier C., Bourgeois E., Just

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Raymond P.;

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Best Local S
Matches
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INIT_MET 0
ACT_SITE 1
SEQUENCE 585 AA;
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                                                                                                                                                                                                                                                                                                                               ASNS_BRAOL STANDARD; PRT; 585 AA.

p43091;
01-FEB-1996 (Rel. 33, Created)
15-JUL-1998 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ASPARAGINE SYNTHETASE (EUTPAMINE-HYDROLYZING) (EC 6.3.5.4) (GLUT DEPENDENT ASPARAGINE SYNTHETASE).

Brassica oleracea (Cauliflower).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyte euphyllophytes; Spermatophyta; Magnollophyte; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CV. SHOGUN;
Downs C.G., Pogson B.J., D
"An asparagine synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Metabolic regulation of asparagine synthetase gene expression maize (zea mays L.) root tips.";
plant J. 9:1-11(1996).
-!- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE - AMP
PROPHOSPHATE + L-ASPARAGINE BLOSYNTHES:
-!- PATHMAX: ASPARAGINE BLOSYNTHES:
-!- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMINE
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PFAM; PF00733; Asn_synthase; 1.
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PROSITE: PS00443; GATASE_TYPE_II: 1.
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                                                                                    CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE. PATHWAY: ASPARAGINE BIOSYNTHESIS. SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMIDOTRANSFERASES. SIMILARITY: TO OTHER ASN SYNTHETASES.
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                                                                                                                                                                                         ) Plant Gene Register PGR95-016 CATALYTIC ACTIVITY: ATP + L-AS
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SIMILARITY: TO OTHER ASN SYNTHETASES
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0 BY SIMILARITY.

1 GATASE (BY SIMILARITY).

66446 MW; 095CE2F99973797E CRC64;
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e cDNA clone
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Pred. No. 3
2; Mismat
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from Broccoli
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3.25e-01;
                                                                                                                                     TYPE-2 GLUTAMINE
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Best Local &
Matches
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PFAM: PF00310; GATASS=_2; 1.

PFAM: PF00733; Asn_synthase; 1.

Ligase; Asparagine blosynthesis: Glutamine amidotransferase.

ACT_SITE 1 1 1 GATASE (BY SIMILARITY).

ACT_SITE 1 1 1 A773083B98A22FE6 CRC64:
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                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                 322 TPMFLMSRK 330
1 TPMFLLSRN
                                                                Similarity 77.8%, 7; Conservative
9
                                                                                  56.5%;
77.8%;
                                                              Score 61;
Pred. No.
2; Misma
                                                                  Mismatches
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3.25e-01;
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                                                                                                  Length 585
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Search completed: Sat May 13 07:12:43 2000 Job time : 90 secs.

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RESULT 1
ID 035902;
AC 035902;
AC 01-JAN-1998 (TIEMBLIEL 05, CIDT 01-JAN-1998 (TIEMBLIEL 12, La DI 01-JAN-1998 (TIEMBLIEL 12, La DI 01-JAN-1999 (TIEMBLIEL 12, La DI 01-JAN-1999 (TIEMBLIEL 12, La DI 01-JAN-1999 (TIEMBLIEL 12, La DI 01-JAN-1999 (TIEMBLIEL 12, La DI 01-JAN-1999 (TIEMBLIEL 12, La DI 01-JAN-1991)

GN DSG3.
OS Mus musculus (Mouse).
OC Eukharia; Metazoa; Chordata; OC Eukharia; Rodentia; Sciurognat RN [1]
CE EUKHARIA; RODENTIA; Sciurognat RN [1]
CE SUBCIECE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
CSTRAIN-BALB/C;
RA ISHIKAWA H./ LI K., UITTO J.;
RA ISHIKAWA H./ LI K., UITTO J.;
RA ISHIKAWA H./ LI K., UITTO J.;
RA SUBCILULAR LOCATION: TYPI DR SUBCILULAR LOCATION: TYPI DR EMBL; U86016; AAB65091.1; -.
DR HSSE; P15116; INCJ.
DR PFAM; PFO0028; Cadherin; 4
DR PFAM; PFO0028; Cadherin; 4
DR PFAM; PFO0028; Cadherin; 5
FT NON_TER 993
SQ SEQUENCE 993 AA; 107888 MW
                 RESULT
ID QS
AC QS
DT 011
DT 011
DT 011
DT 011
DE PF
GN PC
OS HC
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Best Local Similarity 85.7%;
Matches 12; Conservative
Q9YSC2 PRELIMINARY; PRT; 878 AA.
Q9YSC2;
Q9YSC2;
Q1-NOV-1999 (TIEMBLrel. 12, Created)
Q1-NOV-1999 (TIEMBLrel. 12, Last sequence update)
Q1-NOV-1999 (TIEMBLrel. 12, Last annotation update)
PROTOCADHERIN GAMMA C5 SHORT FORM PROTEIN.
PCDB-GAMMA-C5.
PCDB-GAMMA-C5.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-BALB/C;

SITRAIN-HALB/C;

ISHIKAWA H., LI K., UITTO J.;

SUBMITTED (JAN-1997) to the EMBL/GenBank/DDBJ databases.

1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

EMBL; U86016; AAB65091.1; -.

HSSP; P15116; INCJ.

HSSP; P15116; INCJ.

PROSITE; PS00232; CADHERIN; 2.

PRAM; PF00028; cadherin; 4.

Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat.

NON_TER

993

993

SEQUENCE

993 AA; 107888 MW; 881794BD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                          207 SMFLISRNTGEVRT 220
:|||:|||||||
2 PMFLLSRNTGEVRT 15
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Last sequence update)
Last annotation update)
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Pred. No. 4.79e-08; 
2; Mismatches 0; Indels
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RESULT 3
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AC 09Y5F6;
DT 01-NOV-1999 (
DT 01-NOV-1999 (
DT 01-NOV-1999 (
DE PROTOCADHERIN
GN PCDH-GAMMA-C5
OS Homo sapiens
OC Eukaryota; Me
OC Eutheria; Pri
RN [1]
RP SEQUENCE FROM
RC TISUE-BRAIN;
RX MEDLINE; 9930;
RA WU Q., MANIAT
RT "A STITKING o
RT 11ke Cell adh
RL Cell 97:779-7
CC -1- SUBCELLUL
DR PROSITE; PS030
KW Cell adhesion
SQ SEQUENCE 94
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Best Local S
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MEDLINE; 99308635.

WU O., MANIATIS T.;

"A striking organization of a large family of hum
like cell adhesion genes.";

Cell 97:779-790(1999).

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
EMBL; AF152526; AAD43786.1; -.

PROSITE; PS00232; CADHERIN; 5.

Cell adhesion; Glycoprotein; Transmembrane; Calci
SEQUENCE 878 AA; 95192 MW; 07F807CA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; yyyuuu...
WU Q., MANIATIS T.;
A Striking organization of a large family of human neuro.
1 ke cell adhesion genes.";
Cell 97:779-790(1999).
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILAR)
EMBL; AF152339; AAD43733.1; -.
PROSITE; PS00232; CADHERIN; 5.
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding;
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding;
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding;
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding;
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                                                                 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditida; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; C
Eutheria; Primates; Catarrhini;
   Submitted
                                    ANDERSON K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               618
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Similarity 69.2%;
9; Conservative
   (JUL-1995)
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   the
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Pred. No.
3; Misma
                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
N ZK177.6 IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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   EMBL/GenBank/DDBJ
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Pred. No. 2.
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2.77e-02
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   databases
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01-NOV-1996 (TrEMBLrel.
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EMBL; U21321; AAB36970.1; -.
WORMPEP; ZK177.6; CE02095.
PFAM; PF00400; WD40; 1.
                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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"Nucleotide sequence of a 13.9 kb;
plasmid of Salmonella typhimurium:
blosynthetic genes.";
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L; L08613; AAC36963.1;
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273970; CAA98248.1; -.
277664; CAA98248.1; JOINED.
277664; CAB01217.1; -.
273970; CAB01217.1; JOINED.
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SUBMITTED (MAR-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022117; CAA17925.1; -.
PFAM; PF00733; Asn_synthase; 1.
PFAM; PF00731; GATase_2; 1.
PFAM; PF00310; GATase_2; 1.
PFAM; PF00310; GATase_2; 1.
PFAM; PF00310; GATase_1: 1805CB15 CRC32;
PFAM; PF00310; GATase_2; 1.
PFAM; PF00310; GATase_2; 1.
PFAM; PF00310; GATase_3; 1805CB15 CRC32;
PFAM; PF00310; GATase_3; 1805CB15 CRC32;
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LAM H.M., HSIEH M.H., CORUZZI G.M.;
LAM H.M., HSIEH M.H., CORUZZI G.M.;
"Reciprocal regulation of distinct asparagine.
light and metabolites in Arabidopsis thaliana.
Plant J. 0:0-0(1998).
EMBL; AF095452; AAC72836.1; -.
MENDEL; 34482, Arath; 1042; 34482.
SEQUENCE 578 AA; 65223 MW; 8C46069E CRC32;
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SPBC119.10.
SChlzosaccharomyces pombe (Fission yeast).
Schlzosaccharomycets; Ascomycota; Archiascomycetes;
Eukaryota; Fungi; Ascomycota; Archiascomycetaceae;
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042902;
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01-JUN-1998 (TIEMBLIEL 10,
01-MAY-1999 (TIEMBLIEL 10,
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eudicotyledons; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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01-MAY-1999 (TIEMBLTel. 10, L
01-NOV-1999 (TIEMBLTel. 12, L
ASPARAGINE SYNTHETASE.
ASN2.
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Plant J. 0:0-0(1998).
EMBL; AF095453; AAC77837.1; -.
MENDEL; 34483; Arath;1042;34483.
SEQUENCE 578 AA: KEATT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09ZST6;
01-MAY-1999
01-MAY-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                     Ligase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                            EMBL; 077678; AAC49613.1; -. HSSP; P17169; 1GMS.
MENDEL; 8141; Glyma:1042:8141.
PFAM; PF00733; ASn_synthase; 1.
PFAM; PF00310; GATASE_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 10
PRELIMINARY: PRT; 581 AA.
P93167;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1999 (TREMBLREL. 12, Last annotation update)
ASPARAGINE SYNTHETASE 2 (EC 6.3.5.4) (ASPARAGINE SYNTHETASE
(GLUTAMINE-HYDROLYSING)) (ASPARAGINE SYNTHETASE
(GLUTAMINE-HYDROLYSING)).
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MEDLINE; 97188563
HUGHES C.A., BEARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetase in soybean.
Plant Mol. Biol. 33:30
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUGHES C.A., BEARD H., MATTHEWS B.
"Molecular cloning and expression
"Molecular cloning and expression":
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TISSUE-MATURE
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                                                                  322 TPMFLMSRK 330
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   <u>بــر</u>
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CATALYTIC ACTIVITY: ATP + L-AS
DIPHOSPHATE + L-ASPARAGINE + L
TPMFLLSRN
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7; Conser
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Similarity 77.8%;
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larity 77.8%;
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Last sequence update)
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Pred. No. 6.17e-01;
2; Mismatches 0;
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Pred. No. 6.17e-01;
2; Mismatches 0;
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RESULT 13
ID 993618 PRELIMINARY;
AC P93618;
OT 01-MAY-1997 (TIEMBLIED 03, CI
DT 01-MAY-1997 (TIEMBLIED 03, LE
DT 01-WOV-1999 (TIEMBLIED 12, LE
DT 01-WOV-1999 (TIEMBLIED 12, LE
DT 01-WOV-1999 (TIEMBLIED 13, LE
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Matches
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KIM H.-B., AN C.-S.;

SUDMITTED (APR-1998) to the EMBL/G

EMBL; AF061740: AAC16325.1; -.

MENDEL; 29685; Elaum:1042;39685.

PFAM; PF00733; ASN_Synthase; 1.

PFAM; PF00310; GATASE_Z; 1.

SEQUENCE 585 AA; 65878 MW; 8A1
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65329; PRELIMINARY;
065329; (TIEMBLIEL 0
01-AUG-1998 (TIEMBLIEL 0
01-AUG-1998 (TIEMBLIEL 0
01-NOV-1999 (TIEMBLIEL 0
ASPARAGINE SYNTHETASE.
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TISSUE-ROOT
KIM H.-B., A
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SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukhryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyliophytes; Spermatophyta; Magnoliophyta; eudicotyledons; eoore eudicots; Rosidae; eurosids I; Rosales; Elaeagnaceae; Elaeagnus.
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O9ZS23;

O1-MAY-1999 (TrEMBLrel. 10, Created)

O1-MAY-1999 (TrEMBLrel. 10, Last sequence up

O1-NOV-1999 (TrEMBLrel. 12, Last annotation

ASPARAGINE SYNTHETASE TYPE II (EC 6.3.5.4).

AS2.
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EMBL; AJ009952; CAA08913.1; -.
HSSP; P17169; IGMS.
MENDEL; 34839; Phavu;1042;34839.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo euphyllophytes; Bermatophyta; Magnollophyta; eudicotyledons euphyllophytes; Bermatophyta; edicots; Rosidae; eurosids I; Fabales; Fabaceae; Papil
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OSUNA D., GALVEZ G., PINEDA M., AGUILAR M.;
"RT-PCR cloning and expression of a cDNA encoding
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larity 77.8%;
Conservative
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77.8%;
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d. No. 6.17e-01;
Mismatches 0;
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PUEHLER A., PERLICK A.M.;
Plant Sci. 124:89-95(1997).
-I- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GI
DIPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.
EMBL; 272354; CAA96526.1; -.
HSSP; P17169; 1GMS.
MENDEL; 11022; Victa;1042;11022.
PFAM; PF00733; Asn_synthase; 1.
PFAM; PF00310; GATase_2; 1.
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Vicia faba (Broad bean).

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XA SHI L., TWARY S. N., YOSHIOKA H., GREGERSON R.G., MILLER S.S.,

RA SHICL, TWARY S. N., UNKEFER P.J., VANCE C.P.;

YA SAMAC D.A., GANTT J.S., UNKEFER P.J., VANCE C.P.;

YI frogen assimilation in alfalfa: isolation and characterization of

an asparagine synthetase gene showing enhanced expression in root

rodules and dark-adapted leaves.";

Plant Cell 9:1339-1356(1997).

REMBL; UB9923: AAB81011.1;

REMBL; UB9923: AAB81011.1;

REMBL; UB9923: AAB81011.1;

RENDEL: 27006; Medsa; 1042; 27006.

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REPAM; PF003310; GATASSe_2; 1.

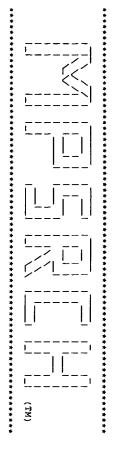
SEQUENCE 586 AA; 66448 MW; 63C8B6BA CRC32;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae;
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MPsrch_pp Run on: protein - protein database search, using Smith-Waterman algorithm Sat May 13 07:22:02 2000; MasPar time 3.01 Seconds 117.993 Million cell updates/sec

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Description: Perfect Score: Sequence: >US-08-991-628-5 (1-15) from US08991628.pep 113 1 CECNIKVKDVNDNFP 15

Scoring table: PAM 150 Gap 15

188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 18.468; Variance 59.453; scale 0.311

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	6	· G	4	w	2	-	Result
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Query Match 100.0%; Best Local Similarity 100.0%; Matches 15; Conservative

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Cytadhesin protein.	CD31 fragment (domains	Segment of desmosomal	•	Amino acid sequence of	Segment of desmosomal	pCTD ORF 4.	Protocadherin clone RA	Plasmodium falciparum	n	Stimulator of iron tra	 S. pneumoniae protein 	0	Human 5' EST secreted	Full length rat cadher	Rat full length cadher	Human cadherin-8.	Full length human cadh	Rat truncated cadherin	Truncated rat cadherin	Protocadherin clone RA	Rat-352 cadherin parti
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disease and which binds to the polypeptide to activate autormatione of the autority of the polypeptide to activate autoreactive T-cells in individuals with the autoimmune disease. This peptide is derived from the human desmoglein 3 protein (amino acids 251-265) and is implicated as a self epitope in pemphigus vulgaris. Peptides derived from the human desmoglein protein are described in w04841-47. Sequence 15 AA;	autoantigen; or an isolated human pathogen polypeptide capable of tolerising an individual to that polypeptide. In both cases, the polypeptide (whether self or non-self) includes an amino acid sequence corresponding to a sequence motif for a MHC class II	Claim 1; Page 40; SBpp; English. Chaim 1; Page 40; SBpp; English. Pharmaceutical preparations for tolerisation to antigens comprise either an isolated human non-collagen or non-myslin basic protein (MBP) polypeptide which is capable of tolerising an individual to an	Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens - useful in disease treatment, and method for identification of other self and non-self antigens implicated in auto-impune disease.	MO9627387-A1. 12-SEP-1996. 07-MAR-1995; US-400796. (HARD) HARVARD COLLEGE. Stromlers JL, Wucherpfennig KW;	W04845; W04845; 18-FEB-1997 (first entry) Self epitope of desmoglein 3, implicated in autoimmune disease. Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris; desmoglein; multiple sclerosis; herpes simplex virus; adenovirus; phosphomannomutase; human papiliomavirus; Epstein-Barr virus; DNA polymerase; infilenza; haemagglutinin; reovirus; sigma protein.	

Homo sapiens.
US7798918-A.
15-DEC-1992.
27-NOV-1991: 798918.
27-NOV-1991: US-798918.
(USSH) US DEPT HEALTH & HUMAN SERVICE.
(USSH) W Klaus-kovtun V, Stanley JR;
Amagai M, Klaus-kovtun V, Stanley JR;
MPI: 93-067415/08.

The protein

of

Human pemphigus vulgaris 130kD antigen. Pemphigus vulgaris; skin disease; autoantibodies; keratinocyte cell surface antigen; glycoprotein;

cell adhesion

R30742 standard; Protein; 999

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pemphigus vulgaris antigen protein extracellular region,
pemphigus vulgaris antigen protein fusion protein; diagnosis;
Autoantibody; immunoglobulin G; IgGl; fusion protein; diagnosis;
Autoantibody; immunoglobulin G; IgGl; blister; skin disease;
treatment; pemphigus vulgaris; PV; bulla; blister; skin disease;
                                                                                                                                                                                                                                                                                                                                      23-JUL-1996.
30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T.
(NISH/) 85-388562/39.
                                                                                                                                                              Fused protein recognised by pemphigus vulgaris auto:antibody - useful to treat and diagnose pemphis vulgaris useful to treat and diagnose pemphis vulgaris (PV) antigen Claim 1; Page 7-9; 9pp; Japanese.

Claim 1; Page 7-9; 9pp; Japanese.

W07908 represents the human pemphigus vulgaris (PV) antigen with w07908 represents the purpose of sa rare extracellular region. The PV antigen is produced in patients with pemphis vulgaris resulting in autoimmune disease. PV is a rare pemphis vulgaris resulting in autoimmune pemphigus vulgaris resulting in suprabasal, intra-epidermal bullae relapsing disease causing suprabasal, intra-epidermal bullae relapsing disease causing suprabasal, intra-epidermal bullae if relapsing disease causing suprabasal to a human IgG1 hinge region untreated. The PV antigen was fused to a human IgG1 hinge region and the resulting fusion protein is useful to treat or diagnose
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                                 250 CECNIKVKDYNDNFP 264
                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CECNIKVKDVNDNFP 15
                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein; 614 AA
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Similarity 100.0%;
15; Conservative
   CECNIKVKDVNDNFP
                                                                      Similarity 93.3%
14; Conservative
                                                                                              90.38;
              15
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pred. No. 3.35e-05;
0; Mismatches 0;
                                                                                Score 102; DB 1;
pred. No. 6.39e-04;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 999;
                                                                                                                         Length 614;
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                                                                                                     Gaps
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L'1115'38

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pr pemphigus foliaceus antigen-IgG constant region fusion protein - linked premphigus foliaceus antigen-IgG constant region fusion protein - linked premphigus foliaceus protein (12: 17pp: Japanese.)

Claim 1: page 10-12: 17pp: Japanese.

CC This sequence represents a fused protein recognised by pemphigus constant region of pemphigus foliaceus patient autoantibody which comprises the constant region of foliaceus foliaceus foliaceus is constant region of pemphigus foliaceus is constant region of pemphigus foliaceus is constant furough the hange portion. Pemphigus foliaceus is constant yen protein through the hange portion seminar fusion constant yen protein fusion recognised by generalised, vesicular and scaling skin eruption similar constant yengent is nested to dermatitis herpetiformis. The pemphigus foliaceus antigen is protein is useful to treat pemphigus foliaceus. The antigen constant is useful to treat pemphigus foliaceus which the fusion protein is immobilised via a carrier. The fusion protein is also useful for detecting pemphigus foliaceus antibodies which is useful construction is defects.

CC useful for detecting pemphigus foliaceus antibodies which is useful constant yengent y
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Best Local S
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DR N-PSDB; T03572.

PT Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat projuccleotide(s) encoding human protocadherins pc3 and pc4 and rat projuccleotide(s) encoding human protocadherins pc3 and pc4 and rat projuccleotide(s) encoding human protocadherin pc3 involved in cell-cell pc3 cellaim 15; page 115-119; 146pp; English.

PS R8685-R86867 represent the sequences for three protocadherins are cc sequence represents the human protocadherin pc3 in these sequences are cc sequence represents the human protocadherin pc3 in vell-cell cc related to cadherin, and possess cell adhesive ability. Cadherins are composed of an N-terminal extracellular domain complete composed of an N-terminal extracellular domain, and a macherine spanning domain, and a cc adherinal cytoplasmic domain. The cytoplasmic domain interacts with the cytoskeleton through catenins and other cytoskeleton associated proteins. Cc cytoskeleton through catenins and other cytoskeleton associated proteins. Cc which possess it, it is essential for the cadherins adhesive function. Cc which possess it, it is essential for the cadherins adhesive function.
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12-SEP-1995;
12-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Homo sapiens.
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WPI; 97-241758/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R86865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R86865 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protocadherin protocadherin; pc3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 CECNIKILDVNDNIP
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26-JUN-1995; U08071.
27-JUN-1994; US-268161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9600289-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           catenin;
                                                                                                                                                                                                                                                                                                                                                                                       Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                DOHE-)
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12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                            INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pc4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pc5; human; rat; cadherin; cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ζ
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Pred.
2; N
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d. No. 1.95e-02;
Mismatches 1;
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pr through, the gastrointestinal tract, e.g. insulin or leuprolide
PS Disclosure; Fig 2: 294pp; English.

CC This sequence is the human HPT-1 protein. The invention relates to
CC purified proteins (I) that bind specifically to at least one of the
CC gastro-intestinal (GI) tract receptors human intestinal
CC peptide-associated transporter (HPTI), hPEPTI, D2H and human
CC sucrose-isomaltase complex (hSI). (I) provide active transport of
CC therapeutic agents through human and animal GI tissue (into the blood)
CC for in vivo delivery, particularly for treatment or prevention
CC of hypertension, diabetes, osteoporosis, haemophilia, anaemia, cancer,
CC insulin or leuprolide, but many other suitable therapeutic agents are
CC disclosed, including genes or inhibitory nucleic acid, imaging agents and
CC antigens. (I) may also provide targeting to the GI tract. Other uses of
CC (in a binding assay); and (ii) to screen for molecules that bind (I).
CC Immunogenic analogues or derivatives of (I) are used to raise antibodies
CC and in immunoassays. The antibodies are used to locate, detect and
CC measure (I), e.g. for imaging, monitoring treatment, tissue analysis
CC etc., also for peptide purification and immobilisation.
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Matches
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Best Local S
Matches 1
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15-MAY-1998. U10088.
15-MAY-1997: US-046595.
(CYTO-) CYTOGEN CORP.
(ELAN-) ELAN CORP PLC.
Alvarez VL, Belinka BA, Cagney GM, Carter JM, Lan Omahony DJ, Patterson CA, Singleton J;
WPI; 99-009568/01.
N-PSDB; X18166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-1999 (first entry)

Human HPT-1 protein sequence.

Gastro-intestinal transport receptor; binding protein; hSI;

B2H; hPEPT1; human; GI tract receptor; sucrose-isomaltase co

intestinal peptide-associated transporter; hypertension; dia

osteoporosis; haemophilia; anaemia; cancer; migraine; angina

therapeutic agent delivery; therapy; probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function via a different method from those with a cytoplasmic domain. These sequences were isolated using primers 1 and 2 (see T03575 and T03576) The proteins may have regulatory functions in the cell, as well as the cell-cell adhesive properties. Antibodies produced against these sequences are useful for modulating the binding activity of these protocadhering, and can be used therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New proteins that bind specifically to receptors in the gastro-intestinal tract and related nucleic acid - chimaeras antibodies, used to deliver therapeutic or diagnostic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protocadherins, an Sequence 787 AA;
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                                     325
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                                     EIHVKVKDINDNPP 338
 ECNIKVKDVNDNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein;
                                                                                            Similarity
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                                                                            Conser
                                                                          51.3%;
64.3%;
vative
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                                                                      Score 58; DB 1; I
Pred. No. 4.32e+01;
3; Mismatches 2
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Pred. No. 1.47e+00;
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                                                                                                           Length 832
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diabetes;
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DR N-85DB; 785401.

PT Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion PS Claim 1; Column 69-72; 56pp; English.

CC This sequence represents human cadherin-5. The invention specifically CC provides details of human cadherin-5, -8, -11, -12 and -13, and rat CC cadherin-8, -5, -11 and -13. Cadherins are calcium-dependent cell CC definesion proteins. They are glycosylated integral membrane proteins CC that have an N-terminal extracellular domain that determines binding specificity, a hydrophobic membrane spanning region and a C-terminal CC cytoplasmic domain, which is highly conserved among members of the superfamily. The C-terminal domain interacts with the cytoskeleton cC superfamily. The C-terminal domain interacts with the cytoskeleton through eatenins and other cytoskeleton-associated proteins. The cover of the converse of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cover of the cov
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08-JUL-1997.
17-APR-1992; 872643.
19-APR-1993; US-049460.
17-APR-1992; US-872643.
01-NOV-1994; US-332638.
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The present sequence is full length human cadherin-5, which is a Ca2+ dependent cell adhesion protein. The human cadherin cDNA was isolated from a placental cDNA library, using probes based on homologous rat cadherin cDNA.

Antibodies or fragments that specifically bind the human cadherin can be used to purify the cadherin, determine its tissue expression and antagonise its ligand/antiligand binding activities.

Sequence 780 AA;
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WPI; 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DOHE-) DOHENY EYE
Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cadherin-5.

Human; cadherin; rat; calcium-dependent cell adhesion protein; superfamily; cytoskeleton; eatenin; cancer.
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03-NOV-1997
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17-APR-1992; US-872643.
19-APR-1993; US-049460.
26-JAN-1994; US-188228.
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Ca2+ dependent; cell adhesion protein; placental; caprain; human; antibody; purification; determination; tissue expression; binding antagonist; calcium ion.
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Suzuki S;
WPI; 97-108328/10.
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larity 81.8%;
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DNA sequence
Oryza sativa.
J10334104-A.
18-DEC-1998.
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Disclosure: Page 16-17: 24pp; Japanese.

The present sequence is used to demonstrate the method of the invention. The specification describes the comparison of DNA base sequences. The method involves 3 steps of: (1) division of a first and second nucleic acid sequence into base groups of three base lengths, and translation into amino acids; (2) all base and amino acid insertions and deletions of the two nucleic acid sequences are observed and the amino acid sequences encoded by these nucleic acid sequences are compared; and (3) adjacent bases and amino acids are compared and step (1) repeated after shifting the translation frame one base towards the 3' end or shifting the translation frame one base towards the 3' end, but the compassing four bases, and not translating the second or third base. The new method is useful for comparing DNA base sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HITA) HITACHI LTD.

WPT: 99-110965/10.

Comparison of DNA base sequences - using accurate observations conservations and deletions and deletions Disclosure; Page 16-17; 24pp; Japanese.

The present sequence is used to demonstrate the method of the deletions and deletions.
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Sequence
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                                                                                                                                                                                                                                  31-JAN-1995 (first entry)
Beta subunit of integrin cell surface receptor.
Integrin; alpha; beta; subunit; glycoprotein; heterodimer;
transmembrane; extracellular matrix; cell signalling; cytoskeleton;
behaviour; signal transduction; receptor.
                                                  modified_site
                                                                                                       modified_site
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31-MAR-1997; JP-079586.
                                                                                                                                                            peptide
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R55273;
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les 9; Conservative
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                                                                      "Potential N-linked glycosylation site.
                                                                                                                                   "N-terminal
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PI Suzuki 5;

DR WPI; 96-068873/07.

DR N-SSDB; T03582.

PT Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat pc5 - involved in cell-cell adhesion and regulation activities pc5 - involved in cell-cell adhesion and regulation activities pc5 - involved in cell-cell adhesion and regulation activities pc5 - involved in cell-cell adhesion.

CC R87102-R87120 represent partial fragments of the rat protocadherin sequence. The cDNAs encoding these sequences were isolated after cC screening a rat brain cDNA preparation with the primers shown in T03575 cC and T03576. The primers were constructed from portions of the amino acid sequences of the third and fourth extracellular domains of published cC cadherin sequences. The full length cDNA sequence encoding rat cC protocadherin pc5 is represented in T03574. The cytoplasmic domain of cadherin interacts with the cytoskeleton through catenins and other corresponding to the complex construction associated proteins. The cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins which do not possess a cadherins adhesive function. The cadherins which do not possess a
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Matches
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Example 5; Figure 9; 34pp; English.

Integrins are heterodimers comrised of alpha and beta subunits, that are non-covalently associated transmembrane glycoproteins. Il alpha chains and 6 beta chains have been recognised in man. Each alpha committed the subunit tends to associate with only one type of beta subunit but there are several exceptions. Integrins mediate (in part) the interaction of cells with the extracellular matrix, forming a link between the extracellular matrix and the cytoskeleton. They may transmit signals from the extracellular to the intracellular environment, affecting cell behaviour. This sequence is the beta4 subunit of an alpha6 beta4 integrin.
                                                                                                                                                                                                                                                                                                          26-JUN-1995; UO
27-JUN-1994; US
(DOHE-) DOHENY 1
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R87107;
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Protocadherin; pc3; pc4; pc5
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WPI; 94-191533/23.
N-PSDB; Q65674.
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01-OCT-1990;
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(QUAR/) QUARANTA V.
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                                                                                                                                                                                          PT Polyniclectide sequences encoding new proto:cadherins - useful PT for modulating natural binding and regulating activities.

Example: Page 38: 114pp: English.

CC Two regions of conserved AA sequence, one from the middle of the CC cterminus of the fourth extracellular subdomain (EC-4) were CC cterminus of the fourth extracellular subdomain (EC-4) were CC designed for use as PCR primers. PCR was carried out on a rat brain CC cDNA preph. Two major bands of about 450 bps and 130 bps were found. CC cDNA preph. Two major bands of about 450 bps and 130 bps were found. CC conservations of the previously identified cadherin sequences. The 450 bp and 130 cc clones were isolated. The DNA and deduced AA sequences of the clones (including sequences corresp. to the PCR primers) are given CC clones (including sequences corresp. to the PCR primers) are given CC clones (including sequences corresp. to the PCR primers) are given CC catherins. The cadherins described thus far have highly conserved CC catherins. The cadherins described thus far have highly conserved CC catherins. The cadherins described thus far have highly conserved CC corresp. Sequences in the EC-3 including the consensus sequence CC v-re or D-Fe located at the middle region of the subdomain and CC corresp. Sequences of other subdomains, except for the Sth extraccellular subdomain (EC-5), are D-R-E and the sequences in R58801 cc little are subdomains include CC corresp. The contrast the deduced AA sequences of the new CC clones that corresp. to cadherin extracellular subdomains include CC corresp. The partial clones are homologous to contrast the deduced AA sequences of the new CC clones that corresp. to cadherin extracellular subdomains include CC correspectively. In contrast the deduced AA sequences of the new CC correspectively conserved to cadherin extracellular subdomains include CC correspectively conserved to conserve the partial clones are homologous to conserve the correspective the sequence of the conserve the correspective the partial clones are h
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WPI; 94
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29-DEC-1992; US-998003
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1 CECNIKVKDVNDNFP 15
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CC This sequence is a H. pylori secreted protein.

CC This sequence is a H. pylori secreted protein.

CC Infection or to identify H. pylori polypeptide binding compounds, in the protein may be used in a vaccine to prevent or treat H. pylori compounds, in the protein as potential H. pylori life cycle activators or inhibitors. The CC useful as potential H. pylori life cycle activators or inhibitors. The CC useful as potential H. pylori life cycle activators or inhibitors. The CC useful as potential H. pylori life cycle activators or inhibitors. The CC acid sequences complementary to the DNA act as antisense sequences and CC can be used to prevent the translation of H. pylori mrNA. Antibodies and acid sequences complementary to the DNA act as antisense sequences and CC and distribution of H. pylori-specific antisens. The genomic sequence of CC and distribution of H. pylori-specific antisens. The genomic sequence of CC use branically shearing the bacterial DNA. The sequences were analysed for the amino acid sequences predicted coding regions CC were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of conterest, particular regions can be isolated from H. pylori by PCR contents and proteins and polypeptide production, e.g. in E. coli posts.
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09-OCT-1997; U05223.
27-MAR-1997; U05223.
06-DEC-1996; US-758118.
29-MAR-1996; US-625811.
02-APR-1996; US-758731.
25-OCT-1996; US-736905.
28-OCT-1996; US-738859.
W09737044-A1.
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(ASTR ) ASTRA AB.
Alm RA, Smith D;
WPI; 97-503122/46.
N-PSDB; V24879.
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Helicobacter pylori.
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02-JUL-1998 (first entry)
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US-736905.
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larity 50.0%;
Conservative
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Pred. No. 1.37e+02;
3; Mismatches 2
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PT Infection and for diagnosis of S. pylori infection
PT Infection and for diagnosis of H. pylori infection
PT Infection and for diagnosis of G. pylori infection
PT Infection and for diagnosis of H. pylori protein of unspecified function.
CC This sequence is a H. pylori protein to prevent or treat H. pylori
CC Infection or to identify H. pylori polypeptide binding compounds,
CC Useful as potential H. pylori life cycle activators or inhibitors. The
CC Useful as potential H. pylori life cycle activators or inhibitors. The
CC Useful as potential H. pylori if cycle activators or inhibitors. The
CC Useful as potential H. pylori if mylori infection. Nucleic
CC acid sequences complementary to the DNA act as antisense sequences and
CC can be used to prevent the translation of H. pylori mRNA. Antibodies
CC and distribution of H. pylori-specific antigens. The genomic sequence of
CC mylori (ATCC 55679) was determined from overlapping contigs generated
CC by mechanically shearing the bacterial DNA. The sequences were analysed
CC defined by computer evaluation. To identify likely H. pylori antigens for
CC vaccine development, the amino acid sequences predicted from various ORF
CC useful antigent for significant homology to other known or exported
CC interest, particular regions can be isolated from H. pylori by PCR
CC interest, particular regions can be isolated from H. pylori by PCR
CC interest, particular regions can be isolated from exported the sequences of
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Matches
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Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-1997.
17-APR-1992; 872643.
17-APR-1992; US-872643.
19-APR-1993; US-049460.
26-JAN-1994; US-188228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DOHE-) D
                                                                                                                                                                                                    Claim 5; Column 112; 59pp; English.

The present sequence is an antigenic epitope from human cadherin-5, which is a Ca2+ dependent cell adhesion protein. Antibodies or fragments that specifically bind the epitope can be used to purify the cadherin, determine its tissue expression and antagonise its ligand/antiligand binding activities.
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1997 (first entry)
Human cadherin-5 antigenic epitope (residues 242-252).
Ca2+ dependent; cell adhesion protein; cadherin; human; antibody;
purification; determination; epitope; tissue expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     w13139 standard; Protein; 11 AA. w13139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alm RA, Smith D;
WPI; 97-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-OCT-1996; US-738859
(ASTR ) ASTRA AB.
Alm RA, Smith D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
US5597725-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding antagonist; calcium ion; antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                      API; 97-108328/10.
Antibodies to cadherin proteins – useful as cadherin antagonists,
                                                                                           Local Similarity
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VTLQDINDNFP 11
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llarity 54.5%;
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                                                      Score 52; DB 1; 1
Pred. No. 1.72e+02;
3; Mismatches
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Pred. No. 1.37e+02;
3; Mismatches 2
                                                                                                                   Length 11;
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Search completed: Sat May 13 07:22:09 2000 Job time : 7 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Sat May 13 07:21:36 2000; MasPar time 4.30 Seconds 164.428 Million cell updates/sec

Description:
Perfect Score:
Sequence: Title: >US-08-991-628-5 (1-15) from US08991628.pep 113

Scoring table:

1 CECNIKVKDVNDNFP 15

PAM 150 Gap 15

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 25.922; Variance 35.935; scale 0.721

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2222244554 32220987654321	Result
113 666 666 667 677 677 677 677	Score
100.0 78.8 55.8 55.8 55.8 53.1 53.1 53.1 53.1 53.1 51.3 51.3 51.3	Query Match
1043 1043 1043 1043 1049 896 896 896 799 2163 226 832 1324 1324 1433 784 784 787	Length
2112211222222222222211	BG BG
IJHUG3 IJHUG1 IJHUG1 S62588 IH64448 IH664448 IH66176 I15858 IT5276 S52484 S55396 S55396 S55396 S55396 IJHUD8 IJHUB8 IJHUB	ID
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S28353	DJV2FP	A69550	в70396	WHRTW	S49116	T02480	G72340	S67593	T12177	A45730	E71008	G64415	C72231	150090	T00588	H75122	E70361	A71232	A36429	JC6319	JC5545
yketi	cted	hypothetical protein	o X		hypothetical protein	•	hypothet	transport protein USO	potassium channel pro	O		pro	ATP synthase F1, subu	carboxypeptidase gp18	hypothetical protein	sarcosine oxidase, ch	۵	hypothetical protein	integrin beta-4 chain	integrin beta-4 chain	integrin beta4E - hum
N		2.42			2.42e+01				1.62e+01	1.62e+01	1.62e+0	1.62e+0	1.62e+0	1.07e+0	1.07e+0	1.07e+0	1.07e+0	1.07e+0	7.09e+0	7.09e+0	7.09e+0

ALIGNMENTS

Ouery Match Best Local Simil Matches 15;	CATION CATION CATION S 5 5 5 6 7 7 7 7 7 7 7 7 8 8 3 9 5 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	ENTRY ENTRY ORGANISM ACCESSIONS # A41088 REFERENCE # authors # Journal # Journal # Litle # L
100.0%; Score 113; DB 1; Length 999; Similarity 100.0%; Pred. No. 1.81e-12; 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	##cross-references GDB:134030; OMIM:169615 p.position 18q12.2 # p.position 18q12.2 # superfamily cadherin; cadherin repeat homology p.Calcium binding; cell adhesion; duplication; glycoprotein; # superfamily cadherin; cadherin; duplication; glycoprotein; calcium binding; cell adhesion; duplication; glycoprotein; # status predicted #label SIG\ # stomain signal sequence #status predicted #label FRO\ # product desmoglein homolog *status predicted *label EXT\ # product desmoglein homolog *status predicted *label CRI\ # stomain cadherin repeat homology #label CRI\ # stomain intransmembrane #status predicted #label INT\ # stomain desmoglein repeat #label DGI\ # stomain desmoglein repeat #label DGI\ # stomain desmoglein repeat #label DGI\ # stomain desmoglein repeat #label DGI\ # stomain site carbohydrate (Asn) (covalent) #status # status predicted #label DGI\ # stomain desmoglein repeat #label DGI\ # stomain desmoglein repeat #label DGI\ # status predicted #label D	ILT 1 IJHUG3 **type complete E desmoglein 3 precursor - human RNATE_NAMES pemphigus vulgaris antigen **tormal_name Homo sapiens *common_name man 30-Jun-1993 **sequence_revision 30-Jun-1993 **text_change 22-Jun-199 A1088 A1088 RENCE A41088 RENCE A41088 Title Anagai, M.; Klaus-Kovtun, V.; Stanley, J.R. Journal Cell (1991) 67:869-877 title Autoantibodies against a novel epithelial cadherin in cross-references MUID:92069753 accession A41088 **molecule_type mRNA **residues 1-99 **label AMA **TICS GDB:DSG3 GDB:DSG3 GDB:DSG3 **TICS GDB:DSG3

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transmembrane protein

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CLASSIFICATION
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                                                                                                                                                          Koch, P.J.; Walsh, M.J.; Schmelz, M.; Goldschmidt, M.D.
Zimbelmann, R.; Franke, W.W.

#journal Eur. J. Cell Biol. (1990) 53:1-12
#title Identification of desmoglein, a constitutive desmosomal glycoprotein, as a member of the cadherin family of addression molecules.
#cross-references MUID:91168965
#accession A48173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       **Eur. J. Cell Biol. (1991) 55:200-208

**title Complete amino acid sequence of the epidermal desmoglein percursor polypeptide and identification of a second ty **Cross-references MUID:92037656**

**arcoss-references MUID:92037656**
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##molecule_type mRNA
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#title Desmoglein shows extensive homology to the cadherin family of cell adhesion molecules.
#cross-references MUID:91097553
#accession A37785
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                                                                                ##molecule_type mRNA
##residues 44-1001,'AQPPSAT' ##label KO3
##cross-references GB:X57784
this sequence has been revised
##note $38721
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##cross-references GB:S64268; GB:S64270
RNCE A37785
                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-1043 ##label KOC ##cross-references EMBL:X58466; NID:g306; PIDN:CAA41380.1; PID:g307
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    #superfamily cadherin; cadherin
calcium binding; cell adhesion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S3872
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30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
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                                                                                                                                                                                                                                                                                                                                     Poynter, D.; Arnemann, J.; Rutman, A.J.; Pidsley, S.C.; Watt, F.M.; Rees, D.A.; Buxton, R.S.; Magee, A.I.

#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:4796-4800
Desmosomal glycoprotein DGI, a component of intercellular desmosome junctions, is related to the cadherin family of cell adhesion molecules.

#Cross-references MUD:91271279
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                                                            ##residues
                                                                             ##molecule_type mRNA
                                                                                                                                                                                                                                                                ##cross-references GB:X56654
                                                                                                                                                                                                                                                                                     ##residues
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Local Similarity 80.0%;
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                                                                                                                                        Wagner, R.M.; Green, K.J.
J. Cell Sci. (1991) 99:809-821
Structural analysis and expression
cadherin-like component of the de
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desmoglein 1 precursor - human
desmosomal glycoprotein I
#formal_name Homo sapiens #common_name man
$10-Jun-1993 #sequence_revision 30-Jun-1993
Wheeler, G.N.; Buxton, R.S.; Parker, Rees, D.A.; King, I.A.; Magee, A.I
                                            A61279
                                                                                                                                                                                                              A61254
Nilles, L.A.; Parry, D.A.D.; Powers,
                                                                                                                                                                                                                                                                                                                               A39706
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wheeler, G.N.; Parker, A.E.; Thomas, C.L.; Ataliotis, P.; Poynter, D.; Arnemann, J.; Rutman, A.J.; Pidsley, S.C.;
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$16906
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#region glycine/serine-rich\
#binding_site carbohydrate (Asn) (covalent) #status
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Pred. No. 9.39e-07
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Best Local Similarity 80.0%;
Matches 12; Conservative
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392-493
392-493
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#title Desmosomal glycoproteins I, II and III: novel members
Cadherin superfamily.
#cross-references MUID:92175187
                                                                                                                                                                                                                                                            #submission
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                                                                                                                                                                           ##status preliminary
##molecule_type DNA
##residues 1-171 ##label MCL
##cross-references EMBL:Z67999; NID:g1067216;
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#p_position 18q12.1-18q12.2
IFICATION #superfamily cadherin; cadherin repeat homology
RDS calcium binding; cell adhesion; duplication; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 CECNIKILDVNDNIP 267
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##residues 1-55 ##label WH3
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CQCSVKIRSVLTDF
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S62588
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35.7%;
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1 1049 #m
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                                                                                     fos/jun DNA-binding domain homology #label FJD #molecular-weight 19348 #checksum 9337
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                            Score 66; DB 2; I
Pred. NO. 8.66e-02;
6; Mismatches 3
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Pred. No. 9.39e-07;
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66-119
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#cross-references MUID:92108053 #accession 841799
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Methanococcus jannaschii.
#cross-references MUID:96337999
##molecule_type mRNA
##residues 1-809 ##label KOC
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Similarity 53.8%;
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                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. (1992) 89:353-357
                                                                                                                                                                                                                                                                                                                                             Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Troyanovsky, R.; Franke, W.W.
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polyferredoxin - Methanococcus jannaschii
#formal_name Methanococcus jannaschii
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
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3; Mismatches 3;
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duplication; glycoprotein; phosphoprotein; transmembrane
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##cross-references EMBL:U12964.1; CESP:F26F4.10
##experimental_source strain Bristol N2
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Similarity 69.2%;
9; Conservative
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Similarity 61.5%;
                                                                                                                                                                                                                                                           *type complete
hypothetical protein F26F4.10 - Caenorhabditis elegans
*formal_name Caenorhabditis elegans
20-Sep-1999 *sequence_revision 20-Sep-1990
T10176
                                               CESP:F26F4.10
17/3; 106/2;
                                                                                                                                                                                    submitted to the EMBL Data Library, March 1996
The sequence of C. elegans cosmid F26F4.
T16176
                             #length 709
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831/3
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T.; Chidgey, M.A.; Garrod, D.R.
J. Cell Sci. (1995) 108:2163-2173
Characterisation of a desmocollin isoform (bovine DSC3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *superfamily cadherin; cadherin repeat homology *length 896 *molecular-weight 99687 *checksum
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19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change
                                                                                                                                                                                                                                    Fulton,
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desmocollin - bovine
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es GB:L33774;
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   52.2%;
                              #molecular-weight
                             175/3; 279/3; 366/1; 401/1; 478/2; #molecular-weight 80477 #checksum
 Score 59;
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Pred. No. 1.28e+00;
1; Mismatches 3
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Pred. No. 1.28e+00;
3; Mismatches 2;
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NID:g914820;
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Length 709
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                         275 ECPIATKTINEEYP 288
                                                                                                                                                                              preliminary ##molecule_type DNA ##residnee
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PIDN:AAB54266.1; GSPDB:GN00021; CESP:R10F2.1
##experimental_source strain Bristol N2; clone R10F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       **status preliminary; translated from GB/EMBL/DDBJ
**molecule_type DNA
**root/Anc-
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##cross-references EMBL:Z56276; NID:g1022345;
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ECNIKVKDVNDNFP 15
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                                                                                                                                                                                                                                                                                                 hypothetical protein SPAC4G8.07c - fission yeast (Schizosaccharomyces pombe)
#formal_name Schizosaccharomyces pombe
16-May-1996 #sequence_revision 13-Mar-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34/1; 114/3; 735/3; 1552/2; 1800/3; 1865/3; 1911/3; 2108/2; 2150/3 #molecular-weight 238609 #checksum 71
                                                                                                                                                                                                                      S62484
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                                                                                                                                                                                                                                                                            S6248
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Pred. No. 3.05e+00;
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3; Mismatches 4
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#authors
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##cross-references EMBL:D30788; NID:g577659; PID:d1007025; PID:g603501
CLASSIFICATION #superfamily conserved hypothetical P115 protein
SUMMARY #length 1324 #molecular-weight 150593 #checksum 3330
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Best Local
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Best Local Similarity 64.3%;
Matches 9; Conservative
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#journal EMBO J. (1994) 13:4938-4952
#title Fission yeast cut3 and cut14, members of a ubiquitous protein family, are required for chromosome condensation and segregation in mitosis.
#cross-references MUID:95045386
#cross-references MUID:95045386
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##residues 1-83;
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D.; Goessner, R.; Tauber, R.
submitted to the EMBL Data Library, December 1994
Molecular cloning of human LI-cadherin:evidence for
type of cadherin within the cadherin superfamily.
$55396
                                                                                                    E70378 *type complete
DNA replication protein Dnac -
stormal_name Aquifex acolicus
08-May-1998 *sequence_revision
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cut3 protein - fission yeast (Schizosaccharomyces pombe
*formal_name Schizosaccharomyces pombe
15-Jul-1995 *sequence_revision 01-Sep-1995 *text_change
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#length 832 #molecular-weight 92207
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15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change
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G.; Warren, P.V.; Gaasterland, A.L.; Graham, D.E.; Overbeek,
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Pred. No. 3.05e+00;
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Pred. No. 3.05e+00;
3; Mismatches 2
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Matches 6; Conservative
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Best Local Similarity 63.6%;
Matches 7; Conservative
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#journal Nature (1998) 392:353-358
#title The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

#cross-references MUID:98196666
#accession E70378
                                                                                                                                                                                                                                                                                               #gene
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                                                                                                               198 CECNLGYKDIDE 209
                                                                                                                                                                                                                                                                                                                                 ##status preliminary
##molecule_type DNA
##residues | 1-656 ##label BEV
##cross-references EMBL:AL049914; GSPDB:GN00062; ATSP:F6E21.20
##experimental_source cultivar Columbia; BAC clone F6E21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type DNA #label AQF ##residues ##resformes GB:AE000713; NID:g2983424; PID:g2983431; GB:AE000657 ##cross-reforences GB:AE000713; NID:g2983424; PID:g2983431; GB:AE000657 ##experimental_source strain VF5
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translation not shown
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Scoring table: PAM 150 Gap 15 Title:
Description:
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1 CECNIKVKDVNDNFP 15

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Mean 26.676; Variance 31.455; scale 0.848

Statistics: pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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EMBL; M76482; AAA60230.1; PIR; A41088; IJHUG3. HSSP; P09803; IEDH. MIM; 169615; PROSITE; PS00232; CADHERIN; 3. PFAM; PF00028; Cadherin; 4. Cell adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein;	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	(POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL). IDISEASE: PEMPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN OTHER FOR THE PROPERTY OF THE COURT AS THE RESULT OF THE DISEASE IN WHICH EPIDERWAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3. AGAINST DSG3.	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 92069753. Amagai M., Klaus-Kovtun V., Stanley J.R.; Amagai M., Klaus-Kovtun V., Stanley J.R.; Antoantibodies against a novel epithelial cadherin in pemphigus "Autoantibodies against a novel epithelial cadherin in pemphigus vulgaris, a disease of cell adhesion."; Cell 67:869-877(1991). Cell 67:869-877(1991)!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS!- FUNCTION: THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN!- CARCINOMAS!- CARCINOMAS.	DSG3_HUMAN STANDARD; PRT; 999 AA. p32926; p32926; color-1993 (Rel. 27, Created) color-1993 (Rel. 27, Last sequence update) color-1997 (Rel. 35, Last annotation update) color-01-NOV-1997 (Rel. 35, Last annotation update) color-02-1997 (Rel. 35, Last annotation update) color-03-1997 (Rel. 35, Last annotation update) color-03-1997 (Rel. 37, Last sequence update) color-03-1993 (Rel. 27, Last sequence update) color-03-1993 (Rel. 27, Created) color-03-1993 (Rel.

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Bos taurus (Bovine).
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adhesion molecules.";
Blochem. Blophys. Res. Commun. 173:1224-1230(1990).

-I- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNC INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND FILAMENTS MEDIATING CELL-CELL ADHESION.
                                                                                                              "Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene. Eur. J. Cell Biol. 55:200-208(1991).
                                                                                                                                                         MEDLINE: 92037656.
Koch P.J., Goldschmidt
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"Identification of desmoglein, a glycoprotein, as a member of the
                                                                                                                                                                                                                                                                                   SEQUENCE OF 44-1043 FROM N.A. TISSUE-MUZZLE EPITHELIUM;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
KOCh P.J., Goldschmidt M.D.,
                                                      Goodwin L., Hill J.E., Raynor K., Raszi "Desmoglein shows extensive homology to
                                                                            SEQUENCE OF 44-493 FROM N.A. MEDLINE; 91097553.
                                                                                                                                                Franke W.W.;
                                                                                                                                                                                                                   molecules.";
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Koch P.J., Walsh M.J.,
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TISSUE-KERATINOCYTES;
MEDLINE; 91271279.
Wheeler G.N., Parker A.E., Arnemann J., Rutman A.J., P.
Buxton R.S., Magee A.I.;
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TRANSMEM
DOMAIN
                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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EMBL; X57784; CAA40930.1; -.
E.ABL; M58165; AAA62709.1; -.
PIR; S14603; IJBCG1.
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TISSUE SPECIFICITY: EPIDERMIS, MUZZLE, TONGUE AND
DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
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adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                             (Rel. 27, Created)
(Rel. 27, Last sequence update)
(Rel. 35, Last annotation update)
1 PRECURSOR (DESMOSOMAL GLYCOPROTEIN
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  glycoprotein
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larity 80.0%;
Conservative
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Pred. No. 2.23e-08;
2; Mismatches 1
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DESMOGLEIN REPEAT 1

DESMOGLEIN REPEAT 2

DESMOGLEIN REPEAT 4

DESMOGLEIN REPEAT 4
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GLY/SER-RICH.
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DESMOGLEIN 1.
EXTRACELLULAR
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MW; ADE46133F8B77C11 CRC64;
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CYTOPLASMIC
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component of intercellular desmosome
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                                                 Ataliotis P., Watt F.M., Rec
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Best Local
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                                                 PCR1_SCHPO STANDARD; PRT; 171 AA.

009926;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
TRANSCRIPTION FACTOR PCR1 (TRANSCRIPTION FACTOR MTS2).
PCR1 OR MTS2 OR SPACZIEI1.03C.
Schizosaccharomyces pombe (Fission yeast).
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
MEDLINE;
Watanabe
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  junctions, is related to the cadherin family of cell molecules.";

Proc. Natl. Acad. Sci. U.S.A. 88:4796-4800(1991).

-!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JU INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AN FILAMENTS MEDIATING CELL-CELL ADHESION.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND
                                           Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Cell adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein;
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SIGNAL 1
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les 12; Conse
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                                                                                                                                                                                           CECNIKVKDVNDNFP
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                       FROM N.A.
 96140438.
Y., Yamamoto
                                                                                                                                                                                                                                                                                                                   CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                    78.8%;
larity 80.0%;
Conservative
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                                            Schizosaccharomyces
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DESMOGLEIN 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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POTENTIAL.
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Best Local
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002213;
15-FEB-2000 (Rel. 39, Created)
15-FEB-2000 (Rel. 39, Last seque
15-FEB-2000 (Rel. 39, Last annot
PUTATIVE G PROTEIN-COUPLED RECER
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EMBL; U87870;
EMBL; Z67999;
HSSP; P05412;
                                                      SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                            Baynes C
                                                                                                                                                Eukaryota; Metazoa; Nemat
Rhabditina; Rhabditoidea;
                                                                                                                                                                                                         Caenorhabditis elegans
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PROSITE; F
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"A heteromeric protein that binds to a meiotic homologous recombination hot spot: correlation of binding and hot spotsivity.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: HETERODIMER OF PCR1/MTS2 AND ATF1/MTS1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation; Activator; DNA-binding; Nuclear protein;
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ed (FEB-1997) t
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ON: INVOLVED IN REGULATION PMENT. BINDS AND ACTIVATES
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171 AA;
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AAB46991.1; -.
CAA91968.1; -.
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the EMBL/GenBank/DDBJ databases
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                                                                                                                                            »da; Secernentea; Rhabditia; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                   sequence update) annotation update) RECEPTOR C02D4.2.
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Pred. No. 1.19e-02;
6; Mismatches :
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9922FDDDFE150BDE CRC64;
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Submitted (NOV-1996)

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Best Local S
Matches
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01-FEB-1994
15-JUL-1998
DESMOCOLLIN
"Complexity and expression patterns of the desmosomal cadherins.";
Proc. Natl. Acad. Sci. U.S.A. 89:353-357(1992).
-i- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERWAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS.
                                                                                                          TISSUE-MUZZLE EPITHELIUM; MEDLINE; 92108053. Koch P.J., Goldschmidt M.
                                                                                                                                                                                      Eukaryota;
Eutheria; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WORMPEP; C02D4.2; CE07837.

PROSITE; PS00237; G_PROTEIN_RECEPTOR; PFAM; PF00001; 7tm_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                 Bos taurus
                                                                                                                                                                                                                                                                                                                       DSC2_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-protein
DOMAIN
                                                                                                                                                                           Bovinae; Bos.
                                                                                                                                                                                                                                           (FRAGMENT)
                                                                                                                                                                                                                                                                                                           P33545;
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SUBCELULIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
MOST SIMILAR TO INSECT OCTOPAMINE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                          CNIKVKDVNDN
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6; Conse
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1 49
50 72
73 82
73 82
73 83
104
120 136
137 157
158 177
158 177
158 200
201
225 244
225 246
247 373
                                                                                                                                                                                      ; Metazoa; Chordata; Craniata; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                 (Bovine).
                                                                                                                                                                                                                                                     (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 36, Last annotation update)
2A/2B PRECURSOR (EPITHELIAL TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448
                                                                                                                                                                                                                                                                                                                                                                                                                            54.9%;
larity 54.5%;
Conservative
                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                          M.D.,
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1 (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
7 (POTENTIAL).
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Pred.
5; M
                                                                                                           Zimbelmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
BY SIMILAR
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CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         62; DB 1; 1
No. 9.47e-02
                                                                                                                                                                                                                                                                                                                      863
                                                                                                                                                                                   Pertebrata; Mammalia;
Pecora; Bovoidea; Bovidae;
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                                                                                                         Troyanovsky
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Best Local
SEQUENCE FROM MEDLINE; 95403
                                                                                                                                                        DSC3_BOVIN STANDARD; PRT; 896 AA. 028060; Q28061; Q28176; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-FEB-2000 (Rel. 39, Last annotation update) DESMOCOLLIN 3A/3B PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
SEQUENCE
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CARBOHYD
VARIANT
VARIANT
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REPEAT
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TRANSMEM
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REPEAT
REPEAT
                                                                                           Eukaryota;
Eutheria;
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EMBL; M81190; AAA30783.1;
PIR; A41799; IJBODC.
PIR; B41799; IJBODD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                          Bovinae;
                                                                                                                              Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00028; cadherin; 5. Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The European Bioinformatics Institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                 295 CIINIEDVNDNLP
                                                                                                                                                                                                                                                                                                                              3 CNIKVKDVNDNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - SUBCELLULAR |
- ALTERNATIVE |
- ALTERNATIVE |
- TISSUE SPECI
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                   95403557.
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                          Bos.
                                                                                         ; Metazoa; Chordata; Craniata; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      810
863
                                                                                                                              (Bovine).
 Holton
                                                                                                                                                                                                                                                                                                                                                                                                 53.1%;
larity 61.5%;
Conservative
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PRODUCTS: FORMS 2A (SHOWN HERE) AND 2B
SPLICING OF THE SAME GENE.
IFICITY: ESOPHAGUS AND RUMEN. WEAKLY IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY
J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          863
95874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE BOUND BY THE CADHERIN-LIKE
 Clarke J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₹:
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
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CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
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POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISSING (IN ISOFORM 2B).
603854CCA16727F2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVQQCDQDNTH
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                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      60; DB 1;
No. 2.60e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            embrane; Repeat;
Calcium-binding
 Hyam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                     Pecora; Bovoi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> ESIRGHTLVKN
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J.L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 863;
                                                                                         Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                         Mammalia;
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Hashimoto

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                        밁
                                                                                                    reflecting epithelial cell proliferation and differentiation.";

RL J. Cell Biol. 126:507-518(1994).

CC --- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED

CC MEDIATING CELL-CELL ADDESION. MAY CONTRIBUTE TO EPIDERWAL CELL

CC ADDESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENTIAL

CC --- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC --- ALTERNATIVE PRODUCTS: FORMS 3A AND 3B ARE PRODUCED BY ALTERNATIVE

SPLICING OF THE SAME GENE.

--- TISSUE SPECIFICITY: STRATIFIED EPITHELIA ONLY (EPIDERWAIS, TONGUE,

ESOPHAGUS AND RUMEN).

1 DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE PEDERMTS.
                                                 Query Match
Best Local S
Matches
                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
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CONFLICT
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REPEAT
REPEAT
                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                    PRINTS: PROVOZOJ, CADHERIN; 3.
PROSITE; PSO0232; CADHERIN; 3.
PFAM; PF00028; cadherin; 5.
Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal; Cell adhesion; Glycoprotein; Calcium-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L33774; AAC41625.1; -.
EMBL; L33774; AAC41626.1; -.
EMBL; X5788; CAA53427.1; -.
HSSP; P09803; ISUH.
                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterisation of a desmocollin isoform (bovine DSC3) exclusively expressed in lower layers of stratified epithelia.";
J. Cell Sci. 108:2163-2173(1995).
                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P09803;
PRINTS; PR002
                                                                                                                                                                                                                                                        REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chidgey M.A.J.,
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    w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY
              CIITVKDSNDNLP
  CNIKVKDVNDNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P.K., Yue K.K.M.,
                                                Similarity 69.2% 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94308280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  686-814 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             05; CADHERIN
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                         352
                                                             53.1%;
69.2%;
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                                                                                                    Œ.
                                                 Score 60; DB 1; I
Pred. No. 2.60e-01;
1; Mismatches 3
                                                                                                                                                              CADHERIN 1.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
POTENTIAL.
POTENTIAL.
                                                                                                             KLHLCNQD -> ESIRGHTG (IN ISOFORM MISSING (IN ISOFORM 3B).
VI -> EF (IN REF. 2).
                                                                                                                                                                                                                                                                                     POTENTIAL.
DESMOCOLLIN 3A/3B.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                        CADHERIN
                                                                                                                                                                                                                                                                    CYTOPLASMIC
                                                                                                                                                    POTENTIAL
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01-NOV-1997 (Rel. 35, L
01-NOV-1997 (Rel. 35, L
PROBABLE ARGINYL-TRNA S
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Q19825;
Q1-NOV-1997
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OBP_HSV6U STANDARD: PRT: 7
P52378: 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
REPLICATION ORIGIN BINDING PROTEIN (OB
U73 OR 19R OR HDRFO.
Lawrence G.L., Nicholas J., Barrell B.G.; "Human herpesvirus 6 (strain Ull02) encodes homologues of the conserved herpesvirus glycoprotein gM and the alphaherpesvirus
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 95266321.
Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.
Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                           "The DNA sequence of human and genome evolution."; Virology 209:29-51(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herpes simplex virus (type 6 / strain Uganda-1102).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding. SIMILAR 252 263 "HIGH" REGION. SEQUENCE 709 AA; 80477 MW; 17587CAA66096B9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WORMPEP; F26F4.10; CE01258.
PRINTS; PR01038; TRNASYNTHARG.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 9514694
Lawrence G.L., N
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|larity 54.5%;
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SYNTHETASE (EC 6.1.1.
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Pred. No. 4.27e-01;
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                                                                                                                                                                                                                                                                                                          coding content,
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 35, Last seque
01-NOV-1997 (Rel. 35, Last annot
REPLICATION ORIGIN BINDING PROTI
U73 OR CH6R.
                                                                          NP_BIND
                                                                                     EMBL; L14772; AAB06356.1; -. DNA replication; DNA-binding; NP_BIND 52 59 /
                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Ways by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                      origin-binding protein.";
J. Gen. Virol. 75:147-152(1995).
-:- FUNCTION: PROBABLY INVOLVED IN DNA REPLICATION. BINDS THE ORIGIN
OF REPLICATION (ORI) (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL9,
                                                                                                                                                                                                                                                                                                                                     Lindquester G.J., Inoue N., Stamey F.R., Dambaugh T.R., Frenkel N., Pellett P.E.;
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                   Betaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                             Herpes simplex virus (type Viruses; dsDNA viruses, no
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or send an
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                                                                                                                                                                                                                                              EHV-1 53, AND VZV 51.
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CENSIKVDIVGNGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CECNIKVKDVNDNFP
                       Similarity 53.3%; 8; Conservative
                                                                                                                                         an email to license@isb-sib.ch).
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35, Last annotation update)
BINDING PROTEIN (OBP).
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                     Score 59;
Pred. No.
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Pred.
                                                                         ATP (POTENTIAL).
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ATP (POTENTIAL).
53F4B0E46C9BCB5F CRC64;
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1. No. 4.27e-01;
Mismatches 5;
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Herpesviridae;
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PRINTS; PRO0205; CADHERIN.
PROSITE; PRO0202; CADHERIN; 3
PFAM; PF00028; Cadherin; 5.
Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garrod D.R.;
"Cloning, sequence analysis and expression desmocollin 2 (DSC2), a cadherin-like adhes wol. Membr. Biol. 11:229-236(1994).
                                                                                                                                                                                                                                                                  modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buxton R.S., Wheeler G.N., Pidsley S.C., Marsden M.D., Jenkins N.A., Gilbert D.J., Copeland N.G.;
"Mouse desmocollin (Dsc3) and desmoglein (Dsc1) genes linked in the proximal region of chromosome 18.";
Genomics 21:510-516(1994).
-!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUN
                                                                                                                                                                                                    EMBL; L33779; AAA79177.1;
EMBL; L33779; AAA79176.1;
EMBL; X73885; CAA52089.1;
HSSP; P09803; 1EDH.
                                                                                                                                                                                                                                                                                                                                                      This
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel.
15-JUL-1999 (Rel.
DESMOCOLLIN 2A/2B
                                                                                                                    Alternative
                                                                                                                                                                                                                                                                                                                use
                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no re
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STRAIN-C57BL/6; TISSUE-EMBRYO;
MEDLINE; 95227276.
                                                                                                          SIGNAL
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MEDLINE; 9504832
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                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVE IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS IN THE INTERACTION OF PLAQUE PROTEINE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADMESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALTERNATIVE PRODUCTS: FORMS 2A AND 2B ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.

TISSUE SPECIFICITY: IN ALL EPITHELIA TESTED AND HEART. DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright.
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                                                                                                                    splicing;
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38, Last annotation update)
PRECURSOR (EPITHELIAL TYPE 2
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135
902
694
715
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243
355
                                                                                                                     Cytoskeleton;
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                      POTENTIAL.
CYTOPLASMIC
CADHERIN 1.
                                                                                                                                                             ω
CADHERIN
CADHERIN
                                                                                                                               Transmembrane; Repeat; Signal;
                                                             DESMOCOLLIN 2A/2B.
EXTRACELLULAR (POTENTIAL).
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                                                                                                                    Calcium-binding
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                                    (POTENTIAL)
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sion molecule.";
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) YAD7 SCHPO STANDARD:
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T 01-FEB-1996 (Rel. 33, Created)
T 01-FEB-1996 (Rel. 34, Last sequence update)
T 01-CT-1996 (Rel. 34, Last annotation update)
JE HYPOTHETICAL 59.6 KD PROTEIN C4GB.07C IN CHROMOSOME I.
3N SPAC4GB.07C.
SSCHIZOSACCHAROMYCES pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
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Matches
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Best Local Similarity 42.9%;
Matches 6; Conservative
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CUT3_SCHPO
P41004;
01-FEB-1995
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SEQUENCE
Schizosaccharomyces
                       CHROMOSOME
                                                                                                                                                                                                                                                                 EMBL; Z56276; CAA91208.1; -. PROSITE; PS01230; TRMA_1; 1. PROSITE; PS01231; TRMA_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                         Badcock K. Churcher C.M., Barrell B.G., Rajandream M.A., Walsh Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: TO YEAST ENDO-EXONUCLEASE NUCR (RNCI).
-i- SIMILARITY: SOME, TO THE RNA METHYLTRANSFERASE TRWA FAMILY.
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REPEAT
                                                                                                                                                                                                                    Methyltransferase.
ACT_SITE 479
SEQUENCE 527 AA:
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95 (Rel. 31, Last sequ
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E SEGREGATION PROTEIN
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Matches
                                                                                         CAD5_MOUSE STANDARD; PRT; 783 AA. P55284; P55284; Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN)
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDH5.
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EMBO J. 13:4938-4952(1994)
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"Fission yeast cut3 and cut14, members of a ubique of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the condensation of the con
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SEQUENCE FROM N.A.
MEDLINE; 95045386.
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                                 SYSTEM.
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SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
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                                                                   SEQUENCE FROM N.A.
TISSUE-PLACENTA;
MEDLINE; 97362755.
All J., Llao F., Ma.
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01-CCT-1993 (Rel. 27, Created)
01-CCT-1993 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
15-FEB-2000 (Rel. 39, Last annotation update)
VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN)
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SIGNAL 1
PROPEP 25
CHAIN 46
DOMAIN 46
TRANSMEM 593
All J, Llao F, Martens E., Muller W.A.; "Vascular endothelial cadherin (VE-cadherin): endothelial cell-cell adhesion." Microcirculation 4:267-277(1997).
                                                                                                                                                                   Breviario F., Caveda L., Corada M., Martin-Padura I., Golay J., Introna M., Gulino D., Lampugnani M.G., Del Golay J., Introna M., Gulino D., Lampugnani M.G., Del Golay J., Introna M., Gulino D., Lampugnani M.G., Del Patroctional properties of human vascular endothellal (784/cadherin-5), an endothelium-specific cadherin."; Arterioscler. Thromb. Vasc. Biol. 15:1229-1239(1995).
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PFAM: PF01049; Cadherin_C_term; 1.
Cell adhesion: Glycoprotein: Phosphorylation: Transmembrane:
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PRINTS; PR00205; CADHERIN.
PROSITE; PS00232; CADHERIN;
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cell-cell contacts.";

J. Cell Biol. 118:1511-1522(1992).

J. Cell Biol. 118:1511-1522(1992).

I. Cell Biol. 118:1511-1522(1992).

I. FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

ITHEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. THIS CADHERIN MAY PLAY A IMPORTANT ROLE IN ENDOTHELIAL CELL BIOLOGY THROUGH CONTROL OF THE INTERCELLULAR JUNCTIONS. IT COHESION AND ORGANIZATION OF THE INTERCELLULAR JUNCTIONS IT CHESTON.

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EMBL; U84722; AAB41796.1; -.
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SEQUENCE OF 5-784 FROM
TISSUE-BRAIN;
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Houen G., Ruco L.P., Dejana
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TISSUE SPECIFICITY: ENDOTHELIAL TISSUES AND BRAIN.
SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
DATABASE: NAME-PROW; NOTE-CD guide CD144 entry;
DATABASE: NAME-PROW; NOTE-CD guide CD144 htm.
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adhesion; Glycoprotein; Phosphorylation; Transmembrane;
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cadherin family: evidence for eight new cadherins
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Query Match 50.4%; Score 57; DB 1; Length 784;
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Cyprinoidea; Cyprinidae; Rasborinae; Danio.
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HYPOTHETICAL 24.9 KD PROTEIN C16E8.02 IN CHROMOSOME
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SEQUENCE FROM N.A.

STRAIN-DSM 2661;

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STRAIN-DSM 2661;

MEDLINE; 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

BULT C.J., WHITE O., OLSEN G.J., ZHOU L.M., CLAYTON R.A., GCCAYNE J.D.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GLODEK A.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAMS M.D., REICH C.I.,

VERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,

SCOTT J.L., GEOGRAGEN N.S. M., WEIDMAN J.F., FURMANN J.L., NGUYEN D.,

UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,

KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;

KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
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01-AUG-1998 (TrEMBLrel C
01-NOV-1999 (TrEMBLrel 1
METHYLVIOLOGEN-REDUCING VHUB OR MJ1193
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FRANKLIN J.L., SARGENT T.D.
Dev. Dyn. 206:0-0(0).
-i- SUBCELLULAR LOCATION: T
EMBL; U41419; AAB47406.1;
HSSP; P15116; 1NCJ.
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Q58593;
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HSSP;
ZFIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         jannaschii.";
Science 273:1058-1073(1996)
-!- FUNCTION: FERREDOXINS A
                                                                                                                                                                                                                                    PRINTS;
                                                                                                                                                                                                                                                      PROSITE; PS00198; 4FE4S_FERREDOXIN; PFAM; PF00037; fer4; 6.
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Archaea; Euryarchaeota;
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P00195; ICLF.
MJ1193; -.
                                                                                                                                                                                                                                    F00037; fer4;
PR00353; 4FE
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Similarity 91.7%;
11; Conservative
  transport;
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HYDROGENASE POLYFERREDOXIN
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7.00e-02;
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MEDLINE; 94150718.
WILSON R., AINSCOUGH R
BONFIELD J., BURTON J.
                                                    WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSO
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON I
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEI
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of
"2.2 Mb
"2.2 Mb
elegans.
Nature 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BARDILL S.
Submitted
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Q21920;
Q1-NOV-1
Q1-NOV-1
Q1-NOV-1
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Eukaryota; Metazoa; Nemat
Rhabditina; Rhabditoidea;
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Similarity 53.8%;
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RL Submitted (MAR-1996) to the EMBL; 270886; CAA94615.1; -
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditi
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae;
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EMBL; D78133; BAA19797.1; ...
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PROSITE; PS00636; DNAJ_1; 1.
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"Cloning of dnak and dnaJ homologous
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lochim. Biophys. Acta 1350:235-239(1997).
|- SIMILARITY: TO OTHER PROKARYOTIC DNAJ,
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PF00684; DnaJ_CXXCXGXG;
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Pred. No. 3.06e-01;
6; Mismatches 2;
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O1-NOV-1998 (TIEMBLIEL 08, Created)
O1-NOV-1998 (TIEMBLIEL 08, Last sequence update)
O1-NOV-1999 (TIEMBLIEL 12, Last annotation update)
SYNAPSIN S-SYN-SHORT (FRAGMENT)
Lollgo pealeil (Longfin squid).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Tenanda; Loliginidae; Loligo.
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Submitted (MAR-1998) to the
EMBL; AF055373; AAC24822.1;
HSSP; P17599; 1AUX.
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-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COU MOST SIMILAR TO INSECT OCTOPAMINE RECEPTORS.
EMBL: Z81031: CAB02718.1: -
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SEQUENCE FROM N.A.
BAYNES C.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PUTATIVE G-PROTEIN RECEPTOR.
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
HILFIKER S., SCHWEIZER F.E.,
AUGUSTINE G.J.;
                                                                                                                                                                  SEQUENCE
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WORNPEP; COZD4.2; CE07837.
WORNTE; PS00237; G_PROTEIN_RECEPTOR; 1.
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PRINTS; PR00237;
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01-NOV-1998
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PFAM; PF00028; cadherin; 5.

CELL adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat.
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-1- SUBCELLULAR LOCATION: TYPE I ME EMBL; AJ002299; CAA05309.1; -.
HSSP; P09803; 1SUH.
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Canis familiaris (Dog).
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Loligo pealeii (Longfin squid).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoida;
Myopsida; Loliginidae; Loligo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel 08, Created)
01-NOV-1998 (TrEMBLrel 08, Last sequence up
01-NOV-1999 (TrEMBLrel 12, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01.NOV-1998 (TrEMBLrel. 08, Created)
01.NOV-1998 (TrEMBLrel. 08, Last sequence update)
01.NOV-1999 (TrEMBLrel. 12, Last annotation update)
DESMOCOLLIN TYPE 2 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUGUSTINE G.J.;
"Two Sites of Action for Synapsin Domain E in Regulating Neurotransmitter Release.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BUXTON R.S.;
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                                                                                                                                                                                                                                        306 CIINIDDVNDNLP 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDLINE; 98380123.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense expression of a desmocollin gene in MDCK cells alters esmosome plague assembly but does not affect desmoglein expression.";
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Similarity 61.5%;
8; Conservative
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35.7%;
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X MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

X BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

X GARTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

X GARDNER A., GREEN P., HAAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

X JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

X JONES M., KERSHAW J., KIRSTEN J., MORTIMORE B., O'CALLAGHAN M.,

X LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

X PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

X PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

X PARSON N., WAITH A., SONHAMMER E., STADEN R., SULSTON J.,

XA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

XA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,

T 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

Y elegans.";
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069468;
01-NOV-1996
01-NOV-1996
01-NOV-1998
                                                                                                  EMBL; U13
NON_TER
SEQUENCE
                                                                                                                       "Nucleotide sequence analysis of a 21-kbp region of the genome of human herpesvirus 6 containing homologues of human cytomegalovirus major immediate-early and replication genes."; virology 204:738-750(1994). EMBL; Ull3194; AAA68464.1; -.
                                                                                                                                                                                                                                                                                       Human herpesvirus 6.
Viruses; dsDNA viruses,
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                               STRAIN-U1102;
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          Betaherpesvirinae;
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EMBL: 281587; CAB04709.1;
SEQUENCE 265 AA; 30553
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ
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T06G6.11.
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01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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Pred. No. 1.28e+00;
5; Mismatches 2
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Best Local s
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A. CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPAA A., SAUNDERS D., SHOWNKEEN F., SHOWNKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhahditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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001912; O1-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SIMILARITY TO MULTIPLE CADHERIN-TYPE REPEATS.
                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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"A comparison of the complete DNA sequences between human herpesvirus-6 variant A and B.",
to 1.0:0-0(1999).
J. Virol. 0:0-0(1999).
EMBL; ABOJ1506; BAA78294.1; -.
EMBL; ABOJ1506; BA978294.1; -.
ESQUENCE 780 AA; 89540 MW; 5F3A240A CRC32;
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01-NOV-1999 (TrEMBLIE1.
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                                                                                                            WATERSTON R.;
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MEDLINE; 94150718.
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Viruses; dsDNA viruses,
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nitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
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Similarity 53.3%;
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DR HSSP: P15116: INC1.
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DR PROSTITE: PS00222: CADHERIN: 8.
PPAM: PF00001; 7tm_1: 1.
DR PFAM: PF00001; 7tm_1: 1.
PRIVIS: PF00026: CADHERIN.
Cell adhesion: Glycoprotein: Transmembrane: Calcium-binding: Repeat.
SQ SEQUENCE 2163 AA: 238609 MM: 6C85C652 CRC32:
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated.

Sat May 13 07:29:32 2000;

MasPar time 3.02 Seconds 117.801 Million cell updates/sec

Title: >US-08-991-628-6
Description: (1-15) from US08991628.pep
Perfect Score: 109
Sequence: 1 SARTLNNRYTGPYTF 15

Scoring table: PAM 150 Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseg35 1:genesegp

Statistics: Mean 19.232; Variance 58.683; scale 0.328

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Re

NO.	Score	Query	Length [. B	ID	Description	Pred. No
- :	109	100.0	15	- 3	W04846	Self epitope of desmog	ر د .
N	109	100.0	614	H	W07908	higus vulgar	5.7
ω	109		999	Н	R30742	Human pemphigus vulgar	•
4	56		480	٢	R12099		6.87e+01
տ	56	51.4	516	۲	R12098	portion	6.87e+01
σ	55	50.5	431	,	R97293	e CRF RB1 rece	8.71e+01
7	54	49.5	91	۳	P61040	l region of	1.10e+02
œ	54	49.5	246	_	R40924	Protein able to bind t	1.10e+02
9	54	49.5	428	<u>,,,</u>	W08609	Chimeric MoMLV and Ty3	•
10	54	49.5	429	سا	W08606	MOMLV and	1.10e+02
11	54	49.5	431	٠,	R90575	Rat CRF2-beta receptor	•
12	54	49.5	449	<u>ب</u>	80980M	Chimeric MoMLV and Ty3	1.10e+02
13	54	49.5	1079	۲	Y03163		1.10e+02
14	54	49.5	1196	_	R75189	Osteoinductive retrovi	1.10e+02
15	53	48.6	105	1	W00832		
16	53	œ	105	μ,	W19018	Anti-human FasL antibo	1.40e+02
17	53	œ	653	ب	R37425	IDUA.	1.40e+02
18	53	48.6	2115	ب ـــا	W59276	Rubella virus RA27/3 N	1.40e+02
19	53	œ	2205	۳	R79048	Infectious rubella vir	1.40e+02
20	52	J	105	ب	W52241	Antibody LD1/2-6-3-VL	
21	52	47.7	105	٢	W52243	Antibody LD1/2-6-33-VL	1.77e+02
22	52	47.7	140	۲	Y12798		1.77e+02
23	52	47.7	454	1	R93616	a	1.77e+02

4 4 5 4	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
51	51	51	51	51	51	<u>5</u>	51	51	51	51	51	52	52	52	52	52	52	52	52	52
46.8	46.8	46.8	46.8	46.8	46.8	46.8	46.8		46.8		46.8	47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.7
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W93601 W56572	W56579	R59935	R55209	Y01036	R55211	W72433	W72435	W06443	W96742	Y01034	R25101	W17871	W56557	W56558	W18302	W97701	R04711	Y00156	Y00157	R97842
Tomato Xa21 clone TRK2 Toxin TcdA, encoded by	Fragment of toxin TcdA	VK3 (DQMDY) VL.	Humanised HP1/2 kappa	Anti VLA-4 antibody SV	Humanised HP1/2 light	Transplanted VK sequen	Humanised VK sequence.	HuMc3 VL region.	Light chain variable r		bGRF prodrug analogue	Photorhabdus luminesce	Toxin TcbA, encoded by	Toxin TcbAii, encoded	Photorhabdus luminesce	Staphylococcus aureus	Sequence of guinea pig	Enterococcus faecalis	Enterococcus faecalis	Kaposi's sarcoma assoc
2.23e+02 2.23e+02	2.23e+02	2.23e+02	2.23e+02	2.23e+02	2.23e+02	2.23e+02	2.23e+02	2.23e+02	2.23e+02	2.23e+02	2.23e+02	1.77e+02	1.77e+02	1.77e+02	1.77e+02	1.77e+02	1.77e+02	1.77e+02	1.77e+02	1.77e+02

ALIGNMENTS

ID W04846 standard; peptide; 15 AA.

AC W04846; Tendard; peptide; 15 AA.

AC W04846 standard; peptide; 15 AA.

AC W04846; 1997 (first entry)

DT 18 FEB-1997 (first entry)

DE Self epitope of desmoglein 3, implicated in autoimmune disease;

KW Tolerisation; self-epitope; antigen; T-cell; thymocyte;

KW autoantigen; HAB; human leukocyte antigen; T-cell; thymocyte;

KW autoantigen; user of desmoglein; multiple sclerosis;

KW human papiliomavirus; pastein-Barr virus; DNA polymerase;

KW 12 SEP-1996.

PA (HARD) HARVARD COLLEGE.

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27-NOV-1991; US-798918.
(USSH) US DEPT HEALTH & H
Amagai M, Klauss kovtun V,
WPI; 93-067436/08.
N-PSDB; 035992.
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R30742 standard; Protein;
R30742;
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                                                                                                                                                                                                                                                                                                                     DNA encoding pemphigus vulgaris antigen - useful in proteins for diagnostic and therapeutic uses Disclosure, Fig 7; SOpp; English.
This sequence is the pemphigus vulgaris 130kD antigen. The prote and its encoding DNA may be used in the diagnosis and treatment pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-1993 (first entry)
Human pemphigus vulgaris 130kb antigen.
Pemphigus vulgaris; skin disease; autoantibodies;
keratinocyte cell surface antigen; glycoprotein;
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Sequence 614 AA;
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30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
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J08188540-A.
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Autoantibody; immunoglobulin G; IgGl; fusion protein; diagnosis;
treatment; pemphigus vulgaris; PV; bulla; blister; skin disease;
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US7798918-A.
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15; Conservative
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Similarity 100.0%;
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V, Stanley JR;
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Pred. No. 5.72e-05;
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Pred. No. 5.72e-05;
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21-MAR-1991
17-SEP-1990; 05-2569
18-SEP-1989; US-408339.
01-MAR-1990; US-487181.
(SYNE-) SYNERGEN INC.
WPI; 91-133285/19.
N-PSDB; Q11798.
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17-SEP-1990; 062569.
18-SEP-1998; US-408339.
01-MAR-1990; US-487181.
(SYNE-) SYNERGEN INC.
        R97293 standar
R97293;
R97293;
21-AUG-1996 (
Mouse CRF RB1
                                                                                                                                                                                     Protein from Haemonchus contortus and other nematodes therapeutic and prophylactic agent to protect plants, a humans from parasitic nematode infection.

Disclosure; Fig 49; 209pp; English.

The proteins derived from the nematode DNA may be used vaccines against parasitic infection of plants, humans esp. sheep. MADs may also be raised to provide passive prophylaxis against infection.
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Disclosure, Fig 49; 209pp; English.

The proteins derived from the nematode DNA may be used to vaccines against parasitic infection of plants, humans a esp. sheep. MAbs may also be raised to provide passive to prophylaxis against infection.

Sequence 480 AA;
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Haem 84-1 portion of H.contortus 55A surface protein.
Parasitic nematode; vaccine; Hc.
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R12099;
22-JUL-1991 (first entry)
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N-PSDB; Q11799.
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                                            standard; Protein; 431
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Similarity 54.5%;
6; Conservative
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larity 54.5%;
Conservative
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d. No. 6.87e+01;
Mismatches 3;
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. No. 6.87e+01;
Mismatches 3;
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Corticotropin

releasing factor receptor; CRF-R; corticoliberin;

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Matches
J60248181-A.
07-DEC-1985.
23-MAY-1984; 102685.
23-MAY-1984; JP-102685.
(SHIS ) SHISEIDO KK.
WPI; 86-025462/04.
                                                                                                                                                                                                                                                                                                                                                                                             W09617934-A2.
13-JUN-1996.
06-DEC-1995. U15909.
09-DEC-1994: US-353537.
17-JAN-1995. US-374009.
(SALK ) SALK INST BIOLOGICAL STUDIES.
(SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                   excess CF
Sequence
                                                            Galactose; expression 
Synthetic.
                                                                                                   P61040;
                                                                                                                                                                                                                                                    Mouse corticotropin releasing factor receptor mCRF-RB1 was identified as the product of a cDNA clone (T28972) isolated from a mouse heart library. Recombinant mCRF-RB1 can be expressed in host cells transformed by the cDNA clone. The receptor can be used to identify agonists and antagonists that modulate the signal transduction activity mediated by CRF receptors. It may be administered therapeutically to reduce high ACTH levels caused by
                                                                                                                                                                                                                                                                                                                                      Isolated corticotropin-releasing factor receptor (CRF-R) - used to develop prods. for modulating signal transduction activity mediated by CRF-R
                                                                              N-terminal region
                                                                                          03-JUL-1991
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Pred. No. 8.71e+01;
3; Mismatches 4
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R40924;
17-FEB-1994
                                                                                                                                      W08609 standard; protein; 428 AA.
W08609;
W08609;
16-JUL-1997 (first entry)
Chimeric MoMLV and Ty3 integrase designated AtBmCm.
Moloney murine leukaemia virus; Saccharomyces cerevisiae;
retrotransposon; yeast Ty3; position specific integration
inflammation; cardiovascular; autoimmune; cancer; HIV; hav
Alzheimer's disease; rheumatoid arthritis; chimeric.
Chimeric - Moloney murine leukaemia virus.
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domain
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Claim 13; Page 22; 40pp; English.

The synthetic gene encodes a protein corresponding to an antibody capable of binding to a specific antigen, in this case the HIV-1 tall protein. Many synthetic genes are synthesised, each containing a predetermined nucleotide region encoding the framework regions of the heavy and light chains of antibody and undetermined nucleotide regions which are random sequences. The genes are then used in the construction of vectors which are subsequently used to transform microbes. The proteins thus produced are screened for binding activity to the apposition anticody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibodies; antigen binding proteins; library; Human Immunodeficiency Virus.
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The vector may be used to express heterologous genes from transformed host when galactose is added as a carbon so Sequence 91 AA;
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Antigen-binding
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19-FEB-1993; 102609.
28-FEB-1992; US-843125
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6; Conservative
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Saccharomyces cerevisiae
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28 NOV-1996:
10-MAY-1996: U06727.
10-MAY-1995: US-445466.
(CHIR ) CHIRON VIAGENE INC.
(REGC ) UNIV CALIFORNIA.
Bilachone VW, Dildine SL,
  WO9637626-A1.
28-NOV-1996; U06727.
10-MAY-1996; U06727.
22-MAY-1995; US-445466.
(CHIR ) CHIRON VIAGENE I
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                                                                                                                                                                                                   16-JUL-1997 (first entry)
Chimeric MoMLV and Ty3 integrase designated AmBtCm.
Moloney murine leukaemia virus; Saccharomyces cerevisiae;
retrotransposon; yeast Ty3; position specific integration;
inflammation; cardiovascular; autoimmune; cancer; HIV; haemophilia;
Alzheimer's disease; rheumatoid arthritis; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            tRNA gene expression. N.B. The present sequence is not shown in the specification, made up from the two original sequences as specified, MOMLV \ell
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WPI; 97-021229/02.
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PT mutagenesis; 98pp; English.

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CC The present sequence is a specific example of a chimeric integrase.

CC made up of three domains from MoMiv and Ty3, with at least one domain control of three domains from MoMiv and Ty3, with at least one domain control of the present sequence. This protein can direct integration of a concentrative into a defined region of a target eukaryotic genome. CC As part of gene delivery vehicles and transduction competent cc recombinant retroviral particles it can be useful in somatic cc and germ cell gene therapy (in vivo or ex vivo) of a wide range of CC genetic, infectious, degenerative, inflammatory, cardiovascular and cc autoimmune diseases or cancer. Typical examples of the many potential applications include treatment of HIV infection, haemophilia, Alzheimer's cc disease and rheumatoid arthritis. This protein rather than wild-type cc degree of variation in gene expression, and particularly does not disrupt trake of the present sequence is not shown in the specification, but is cade up from the two original sequences as specified, MoMLV and Ty3, which are shown.
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R90575;
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CRF2-beta receptor; corticotropin-releasing factor-2 receptor;
cerebrovascular disorder; memory disorder; Alzheimer disease.
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Bilachone VW, Dildine S
Sandmeyer SB;
WPI; 97-021229/02.
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therapy, providing more
rates of insertional
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Best Local S
Matches
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28-NOV-1996.
10-MAY-1996: U06727.
22-MAY-1995: US-445466.
(CHIR ) CHIRON VIAGENE INC.
(REGC ) UNIV CALIFORNIA.
Bilachone VW, Dildine SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TT 12
W08608;
W08608;
                                                                                           eukaryotic genomes - useful consistent gene expression
                                                                                                New chimeric integrase for targetted New chimeric integrase for targetted enemies - useful for gene
                                                                                                                                                                                            Bilachone VW,
Sandmeyer SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moloney murine leukaemia virus; Saccharomyces cerevisiae; retrotransposon; yeast Ty3; position specific integration; inflammation; cardiovascular; autoimmune; cancer; HIV; hae Alzheimer's disease; rheumatoid arthritis; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corticotropin-releasing factor-2 receptor, and DNA encoding it used to isolate CRF-2 receptor antagonists for the treatment of cerebrovascular disorders, memory disorders and Alzheimer's disease Disclosure; Page 63-66; 109pp; English.

Rat corticotropin-releasing factor-2-beta (CRF2-beta) receptor (R90575) is a membrane-bound G-coupled protein receptor involved in signal transduction. It can be produced by expression of encoding cDNA (T12244) in procaryotic or encaryotic host cells. Recombinant CRF2 receptor is used to screen CRF2 receptor agonists and antagonists of therapeutic appln., and to prepare antibodies which specifically bind to CRF2 receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lovenberg TW, Olte
WPI; 96-049680/05.
N-PSDB; T12244.
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14-JUN-1995; U07757.
14-JUN-1994; US-259959.
31-JAN-1995; US-381433.
07-JUN-1995; US-485984.
(NEUR-) NEUROCRINE BIOSCIENCES INC.
       The present sequ
                                               mutagenesis
Claim 7; Page -; 98pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUL-1997 (first entry) Chimeric MOMLV and Ty3 int
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moloney murine leukaemia
Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431 AA;
  sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Souza EB,
W, Oltersdorf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- A
/note- "From
62. .304
                                                                                                                                                                                                                                                                                                                                                                                                                                /label B
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305. 449
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/note-
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    is a specific ins from MoMLV
                                                                                                                                                                                                                                                                                                                                                             - "From MoMLV"
                                               English
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                                                                                                                                                                                                                  Jolly DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 54; DB 1; I
Pred. No. 1.10e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Туз"
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example of V and Ty3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transposon Ty3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus.
                                                                                              vector integration in therapy, providing more rates of insertional
                                                                                                                                                                                                                  Respess
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                        of.
f a chimeric integrase with at least one domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease
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PS Claim 32: Column 45-52; 70pp: English
CC This sequence represents a murine leukaemia virus (MuLV) reverse
CC transcriptase. The invention relates to a method of producing double
CC transcriptase. The invention relates to a method of producing double
CC murine leukaemia virus reverse transcriptase (xM-MuLV). The method, the
CC murine leukaemia virus reverse transcriptases and nucleic acids disclosed may be
CC cloned, cDNA ilbraries. Use of the method to construct cDNA libraries
CC cloned, cDNA libraries. Use of the method to construct cDNA libraries
CC ensures that the reverse transcriptase is able extend the first strand of
CC the cDNA up to the ultimate 5' end of the mRNA, therefore ensuring that
CC all sequences are represented in the library, whereas previously, some
CC sequences would be lost due to incomplete transcription (e.g. as a result of RNAse
CC of hairpin loop formation) or mRNA degradation (e.g. as a result of RNAse
CC and proteins present in the cell will repair any mistakes or nicks in the
CC and proteins present in the mRNA for insertion into a vector by adding the
CC the method provides a convenient way of priming it for cDNA synthesis. Also,
CC clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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which are shown.
which are 449 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 13
Y03163 standard; protein;
Y03163;
                                                                                                                               Sequence
                                                                                                                                                                 the method clones.
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Ruppert SJ;
WPI; 99-253852/21.
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MULV reverse transcriptase.
MULV reverse transcriptase.
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N.B. The present sequence is not shown in imade up from the two original sequences as
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US5891637-A.
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15-SEP-1997; US-929967.
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                                                         Length 1079
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R75189; 30-MAY-1996 (first entry)

R75189

standard; Protein; 1196 AA

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21-MAR-1996; JP-087420.
20-MAR-1995; JP-087420.
27-OCT-1995; JP-303492.
(SUME ) SUMITOMO ELECTRIC IND CO.
(SUME ) SUMITOMO ELECTRIC IND CO.
Rayagaki N, Nakata M, Okumura K,
WPI; 96-443140/44.
          Claim 28; Page 91; 133pp; Japanese.

Claim 28; Page 91; 133pp; Japanese.

The present sequence is the light chain variable region of the anti-human Fas ligand monoclonal antibody (MAD) NOK-5. NOK-5 is produced by the hybridoma NOK-5 (FERM BP-5048), which was prepared by immunising mice with transformed human Fas ligand expressing COS cells, and fusing spleen cells isolated from the mice with myeloma P3x63Ag8 653 (ATCC CRL-1580) cells. The MAD recognises the human P3x63Ag8 653 (ATCC CRL-1580) cells. The MAD recognises the human fas ligand on the cell surface or in solution, and can be used to inhibit the apoptosis inducing cell surface Fas ligand/Fas reaction. The MAD can also be used for a Fas ligand assay in biological samples (e.g. human blood), especially for disease diagnosis, e.g. hepatitis, infectious mononucleosis and systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAY 1997 (first entry) variable light chain of anti-human Fas ligand antibody NOK-5. Variable region; light chain; human; Fas ligand; monoclonal; antibody; NOK-5; hybridoma; inhibition; apoptosis; assay; diagnosis; disease; hepatitis; infectious mononucleosis; systemic lupus erythematosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; 094266.

RFB-14 retrovirus genome - and prodn. of osteo-inductive proteins Claim 14; Fig 1; 46pp; German.

Claim 14: Fig 1; 46pp; German.

The full-length proviral genomic sequence of retrovirus RFB-14 has been determined. The virus codes for an osteoinductive protein, although the precise location of the coding region has not yet been identified. The virus may be useful in gene therapy of bone growth disorders such as osteoporosis. The present sequence is that of the sequence 1196 AA;
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12-OCT-1995.
05-APR-1994; 411718.
05-APR-1994; DE-411718.
(GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
Erfle V. Gimbel W. Oestergaard M. Pedersen FS.
Schmidt J. Strauss P.
WPI; 95-352078/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1131 TKNLEPRWKGPYT 1143
                                                                                                                                                                                                                                                                                                                                                                                                                     solution
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody specifically for the detection of Fas ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus.
W09629350-Al.
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nes 6; Conservative
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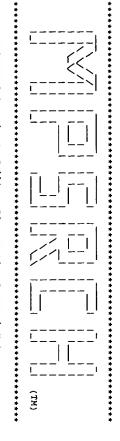
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ş 밁 91 HYSSPYTF 98 œ RYTGPYTF 15

Search completed: Sat May 13 07:29:39 2000 Job time: 7 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Run on:

Sat May 13 07:22:27 2000; MasPar time 96.51 Seconds
4.733 Million cell updates/sec

Title: VJS-08-991-628-6
Description: (1-15) from US08991628.pep
Perfect Score: 109
Sequence: 1 SARTLNNRYTGPYTF 15

Tabular output not generated.

Sequence: 1 SARTLNNRYTGPYTF 15
Scoring table: PAM 150
Gap 15

Searched: 83857 segs, 30454973 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot38 1:swissprot

Statistics: Mean 27.244; Variance 33.691; scale 0.809

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

DR DR DR WW	######################################	1
embrane; Cytoskeleton; Glycoprotein	IND DSG3_HUANN STANDARD; PRT; 999 AA. AC 932926; AC 932926; DT 01-CCT-1993 (Rel. 27, Created) DT 01-CCT-1993 (Rel. 27, Last sequence update) DT 01-NOV-1997 (Rel. 35, Last annotation update) DT 01-NOV-1997 (Rel. 35, Last annotation update) DE DESMOCIEIN 3 PRECURSOR (130 KD PEMPHIGUS VULGARIS ANTIGEN) (PVA). DSG3. OS HOMO sapiens (Human). CE Lutheria: Primates; Catarrhini; Hominidae; Homo. RN [1] RN MEDLINE; 92069753 RA Amagai M., Klaus-Kovtun V., Stanley J.R.; ALCOLORIES, 20069753 RA Amagai M., Klaus-Kovtun V., Stanley J.R.; RY VULGATIS, a disease of cell adhesion."; RY TULGATIS, a disease of cell adhesion." RI TOUCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE CELL FILAMENTS MEDIATRING CELL-CELL ADHESION. CI- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CC SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CC TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, ESOPHAGUS AND CARGINOMAS: (POTENTIAL). CC DIMBASE: PROPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN DISEASE IN WHICH EPIDERMAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3. C SUBCELLULAR CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3. C SINGLARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY. CC SINGLARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY. CC SUBFAMILY: DSSNOSOMAL SUBFAMILY. CC -	

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STRAIN-$288C / AB972;

STRAIN-$288C / AB972;

STRAIN-$288C / AB972;

STRAIN-$288C / AB972;

STRAIN-$288C / AB972;

STRAIN-$288C / AB972;

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                HORST M., Jenoe P., Kronidou N.G., Bolliger L., Oppliger W.,
Scherer P., Manning-Krieg U., Jascur T., Schatz G.;
"Protein import into yeast mitochondria: the inner membrane impor
site protein ISP45 is the MPII gene product.";
EMBO J. 12:3035-3041(1993).
-1- FUNCTION: INVOLVED IN PROTEIN IMPORT INTO THE MITOCHONDRION.
PROBABLY INVOLVED IN TRANSLOCATION ACROSS THE INNER MEMBRANE.
AS A BINDING PROTEIN REQUIRED FOR DRIVING THE IMPORT OF
PREPROTEINS. RECRUITS MITOCHONDRIAL HSP70 AND ITS CO-CHAPERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE: 93010953.

Maarse A.C., Blom J., Grivell L.A., Meijer M.;

*MPII, an essential gene encoding a mitochondrial
is possibly involved in protein import into yeast
EMBO J. 11:3619-3628(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IM44_YEAST STANDARD; PRT; 431 AA.

001852;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MITOCHONDRIAL IMPORT INDER MEMBRANE TRANSLOCASE SUBUNIT TIM44
PRECURSOR (MITOCHONDRIAL PROTEIN IMPORT PROTEIN 1) (INNER MEMBRANE IMPORT SITE PROTEIN 45) (ISP45) (MEMBRANE IMPORT MACHINERY PROTEIN
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Submitted (DEC-1994) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                              MEDLINE: 93345448.
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Partington G., Bomford A., Patient R.;
"Over-expression of GATA-6 in xenopus embryos blocks differentiation
of heart precursors.";
EMBO J. 16:355-368(1997).

-I- FUNCTION: ASSOCIATED WITH CARDIAC SPECIFICATION AND CAN REGULATE
CARDIAC-SPECIFIC TRANSCRIPTION DURING EMBRYOGENESIS. ACTIVATES
THE EXPRESSION OF CARDIAC MHC-ALPHA IN VIVO.

-I- SUBCELLULAR LOCATION: NUCLEAR.
-I- SIMILARITY: BELONGS TO THE GATA-TYPE TRANSCRIPTION FACTOR FAMILY.
                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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EMBL; X67276; CAA47693.1; -.
PIR; S25196; S25196.
SGD; L0001138; MPI1.
Mitochondrion; Inner membrane; Transport; Pro
Translocation; Transit peptide; ATP-binding.
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Batrachia; Anura; Me
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TISSUE-LIVER;
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Fukaryota; Metazoa; Chordata; Craniat
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SIMILARITY: BELONGS TO THE TIM44 FAMILY.
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WORMPEP; C28A5.4; CE05325.
PRINTS; PR00031; HOMEOBOX.
PRINTS; PR00031; HOMEOBOX.1; 1.
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-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE DISTAL-LESS FAMILY OF HOMEOBOX
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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STRAIN-BRISTOL N2;
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1 SARTLNNRYTGPYTF 15
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182
236
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  (Rel.
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102 161 HOMEOBOX.
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                                              STANDARD;
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298
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    16, Created)
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GATA-TYPE.
POLY-SER.
POLY-SER.
POLY-SER.
C93COCDE246204D3 CRC64;
                                                                                                                                                                                                                                           Score 60; DB 1;
Pred. No. 6.23e-01
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Pred. No. 2.41e-01
                                                                                                                                                                                                                                                                                                            18B93FF08C2576EB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                              CBPZ_SIMVI STANDARD; PRT; 304 AA. P42788; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) 2INC CARBOXYPEPTIDASE (EC 3.4.17.-) (FRAGMENT).
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PIR; JQ0658; G8BPT4.
PIR; JF0058; JF0058.
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Viruses; dsDNA viruses,
T4-like phages.
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15-JUL-1999
15-JUL-1999
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00699; NITROGENASE_1_1: 1.
PROSITE: PS00090; NITROGENASE_1_2: FALSE_NEG PFAM; PF00148; oxidored_nitro; 1.
Nitrogen fixation.
SEQUENCE 444 AA; 48332 MW; 766B4886169591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

BUILKERNE W.J., Scappino L.A., Haselkorn R.;

Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: THIS PROTEIN MAY PLAY A ROLE IN THE BIOSYNTHESIS.

THE PROSTHETIC GROUP OF NITROGENASE (FEMO COFACTOR).

-!- PATHWAY: FE-MO COFACTOR BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
ACT_SITE
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SEQUENCE
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METAL
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Hydrolase; Carboxypeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIFN_ANASP
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  (NITROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anabaena sp.
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                                                                                                                                                                                                                                                                                                      h 53.2%;
Similarity 46.2%;
6; Conservative
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(Rel. 38,
(Rel. 38,
(Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 38, Last annotation update)
MOLYBDENUM-IRON PROTEIN ALPHA CHAIN
E COMPONENT I) (DINITROGENASE).
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Pred. No. 1
4; Mismai
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Pred. No.
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ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
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                                                                                                                                 PRT;
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Mismatches 3;
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BIOSYNTHESIS
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9.94e-01;
9.5;
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                  <u>8</u>
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A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
A Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
A Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
A Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
A Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.*;
A Bacteriol. 179:7135-7155(1997).
C -!- FUNCTION: THE KEY ENZYMATIC REACTIONS IN NITROGEN FIXATION ARE
CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
CATALYZED BY THE MOLYSDENUM-IRON PROTEIN.
C -!- CATALYTIC ACTIVITY: 8 REDUCED FERREDOXIN + 8 H(+) + N(2) + 16 ATP
- 8 OXIDIZED FERREDOXIN + 2 NH(3) + 16 ATP + 16 ORTHOPHOSPHATE.
C -!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS THAT BINDS
C -!- SUBULTARTY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                      01-MAR 1989 (Rel. 10, Created)
01-MAR 1989 (Rel. 10, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON 412 (CONTAINS:
PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49);
ENDONUCLEASE).
                                                                                                                                                                                                                                                                                                                              POL4_DROME 
P10394;
"Yuki S., Inouye S., Ishimaru S., Saigo
"Nucleotide sequence characterization c
retrotransposon, 412.";
Eur. J. Biochem. 158:403-410(1986).
                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Trac
Pterygota; Neoptera; Endopterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000916; AAB86037.1; -.
HSSP; P00467; IMIO.
PROSITE; PS00699; NITROGENASE_1_1; FALSE_NEG.
PROSITE; PS00090; NITROGENASE_1_2; 1.
PFAM; PF00148; oxidored_nitro; 1.
Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur.
Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur.
SEQUENCE 469 AA; 52866 MW; 7D2CD5FFED9EC7B8 CRC64;
                                                                      SEQUENCE FROM N.A. MEDLINE; 86274717.
                                                                                                                                                                                                   POL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pred.
2; M
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8 H(+) + N(2) + 10 ...

+ 16 ORTHOPHOSPHATE.
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                                                                                                                                            Muscomorpha;
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Best Local S
Matches
Nuclear
ZN_FING
ZN_FING
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P43693;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
15-JUL-1998 (Rel. 36, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                          PRINTS; PRO0619; GATAZNFINGER.
PROSITE; PS00344; GATA_ZN_FINGER;
PFAM; PF00320; GATA; 2.
Transcription regulation; Activate
                                                                                                                                                                                                                                                                                                                            Burch J.B.E., Evans T.;
"GATA-4/5/6, a subfamily of three transcription in developing heart and gut.";
J. Biol. Chem. 269:23177-23184(1994).
-i- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1193 GHKLDFKYTGPYKI
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PFAM; PF00078; rvt; 1.

Hydrolase; Aspartyl protease; RNA-directed DNA polymerase; Endonuclease; Transferase; Polyprotein; Transposable element. ACT_SITE 63 PROTEASE (BY SIMILARITY).

SEQUENCE 1237 AA; 143041 MW; AC57F1C159D14B65 CRC64;
                                                                                                           EMBL; U11889; AAA57505.1; -. HSSP; P17678; 1GAU.
                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
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HSSP; P03366; 1HEG:
FLYBASE; FB90000006; 412.
PROSITE; PS00141; ASP_PROTEASE;
                                                                                                                                                                      entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-WHITE LEGHORN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATA6
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                                                                                                                                                       send
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                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: MORE ABUNDANT IN STOMACH, AND IN SMALL INTESTINE. LOWER LEVELS IN LUNG, LIVER, OVARY AND HEART. SIMILARITY: BELONGS TO THE GATA-TYPE TRANSCRIPTION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U22.
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 protein.
181
235
                                                                                                                                                       s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Galliformes;
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   205
259
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, Last annotation update)
GATA-6 (GATA BINDING FACTOR-6)
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Phasianidae; Phasianinae; Gallus.
                                             Activator; DNA-binding;
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Pred.
 GATA-TYPE.
GATA-TYPE.
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Biosci. Blotecher'
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CHITIN SYNTHASE A (EC 2.4.1.16) (CHITIN-UDP A)
TRANSFERASE A) (CLASS-II CHITIN SYNTHASE A).
CHSA OR CHS2.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                  PFAM;
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                                                                                                                                                                                                                                                                                                                                                                                                      entitles requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Classification of fungal chitin synthases.";

Proc. Natl. Acad. Sci. U.S.A. 89:519-523(1992).

-I- FUNCTIO: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.

-I- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + [1,4-(N-ACETYL-BETA-D-BETA-D-GLUCOSAMINYL)](N) = UDP + [1,4-(N-ACETYL-BETA-D-
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Eukaryota: Fungi: Ascomycota: Plectomycetes:
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Robbins P.W.,
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                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT 1, MITOCHONDRIAL PRECURSOR
(EC 1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH).
IDH1 OR YNL037C OR N2690.
Saccharomyces cerevisiae (Baker's yeast).
Saccharomyces cerevisiae (Baker's yeast).
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Elzinga S.D.J., Bednarz A.L.,
Grivell L.A.;
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"Subunit structure, expression, and funct isocitrate dehydrogenase in Saccharomyces J. Bacteriol. 172:4280-4287(1990).
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Submitted (MAY-1996)
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01-DEC-1992
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Nucleic Acids Res. 21:5328-5331(1993).
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                                                                                                                                                                                                                                                                                                                                             INCLUDING AMP, NAD+, AND CITRATE.
SUBUNIT: OCTAMER OF TWO NONIDENTICAL SUBUNISUBCELLULAR LOCATION: MITOCHONDRIAL.
SIMILARITY: BELONGS TO THE ISOCITRATE AND DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: PERFORMS AN ESSENTIAL ROLE IN THE OX.
THE CITRIC ACID CYCLE. ALSO BINDS RNA; SPECTIAL
5'-UNTRANSLATED LEADERS OF MITOCHONDRIAL MENAS
CATALYTIC ACTIVITY: ISOCITRATE + NAD(+) = 2-OX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENZYME REGULATION: ALLOSTERICALLY REGULATED
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                                                               ; M95203; AAA34711.1;
; Z71313; CAA95904.1;
S31264; S31264.
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omyces cerevisiae.";
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CONFLICT CONFLICT

Repeat; RNA-binding.
NA -> QR (IN REF. 2).
L -> S (IN REF. 2).
LMKCTYKI -> FEVYI (IN

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L0001294; NUP145

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Mitochondrion: Allosteric e
TRANSIT 1 1
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01-FEB-1996
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                                               EMBL;
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SGD; 1
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N145_YEAST
                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend.an.email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                      Rieger M., Brueckner "Sequence analysis of chromosome VII.";
                                                                                                                                                                                                                                                                                                                                                               Wente S.R., Blobel G.;
"NUP145 encodes a novel yeast glycine-leucine-phenylalanine-glycine (GLFG) nucleoporin required for nuclear envelope structure.";
J. Cell Biol. 125:955-969(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fabre E., Boelens W.C., Wimmer C., "Nupl45p is required for nuclear e. homopolymeric RNA in vitro via a n. Cell 78:275-289(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 94320139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's Eukaryota; Fungi; Ascomycota; Sacc
                                                                                                                                                                                                                                                                             Yeast 13:1077-1090(1997)
                                                                                                                                                                                                                                                                                                                           MEDLINE; 97435481
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STRAIN-ATCC 26109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetaceae;
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                                                                                                                                                                                                                      FUNCTION: MAY PLAY A DIRECT ROLE IN NUCLEOCYTOPLASMIC RNA AND ALSO IN PROTEIN IMPORT. BINDS HOMOPOLYMERIC RN SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX.

DOMAIN: CONTAINS G-L-F-G REPEATS.
                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE GLFG FAMILY OF NUCLEOPORINS
                                                       X76557; CAA54057.1; -. Z32672; CAA83584.1; -. Z72614; CAA96798.1; -.
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(Rel. 33, Last sequence up)
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teric enzyme; RNA-binding.
11 MITOCHONDRION.
60 ISOCITRATE DEHYDROGENASE (NAD) SUBUNIT
03 BINDING TO ISOCITRATE (BY SIMILARITY).
39324 MM; 0932E7B3CD685240 CRC64;
                                                                                                                                                                                                                                                                                                  Schaefer M., Mueller-Auer S.;
3 kilobases from Saccharomyces
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Pred.
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r export of mRNA a
novel conserved
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No. 3.90e+00;
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and binds
d motif.";
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                                                                                                                                                                                                                                                                                                                                                          SULT 15
Y4ZC_RHISN STANDARD;
P55730;
C 01-NOV-1997 (Rel. 35, Created)
T 01-NOV-1997 (Rel. 35, Last sequence update)
O1-NOV-1997 (Rel. 35, Last annotation update)
O1-NOV-1997 (Rel. 35, Last annotation update)
T 01-NOV-1997 (Rel. 35, Last annotation update)
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Best Local Similarity
7; Conser
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Best Local Similarity
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Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alph
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
GVPF/L PROTEIN.
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                                                                          SEQUENCE FROM N.A.
MEDLINE; 97305956.
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal
Perret X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *Genes encoding proteins homologous to halobacterial Gyps N, J, K, & L are located downstream of gypC in the cyanobacterium Anabaena flos-aquae. *;
DNA Seq. 7:97-106(1997).
-- FUNCTION: MAY PLAY A STRUCTURAL OR REGULATORY ROLE IN GAS VESICLE SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                   Rhizobiaceae;
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Bactería; Cyanobactería; Nostocales; Nostocaçeae; Anabaena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVPFL.
Molecular basis of symbiosis between Nature 387:394-401(1997).
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"Genes encoding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                Proteobacteria; alpha subdivision; eae; Rhizobium.
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Pred. No. 6.08e+00;
2; Mismatches 4
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Pred. No. 3.90e+00;
5; Mismatches 2;
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                                   Rhizobium and legumes.";
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Matches
                 Query Match
Best Local Similarity
                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                        EMBL; AE000109; AAB91961.1; -. Hypothetical protein; Plasmid. SEQUENCE 261 AA; 28349 MW;
                                                                                                                                                                                                                                                                                                -i- SIMILARITY: TO P.SYRINGAE (PV. PHASEOLICOLA) AVIRULENCE PROTEIN
AVRPPH3.
   5.
   Conservative
                   50.5%;
                   Score 55; DB 1;
Pred. No. 6.08e+00
                                                                          52939C1919DFEC43 CRC64;
   Mismatches
   2:
                                    Length 261;
   Indels
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238 RSLANRYSNP 247 |:| ||: | 3 RTLNNRYTGP 12

Search completed: Sat May Job time: 108 secs.

13 07:24:15

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 07:24:34 2000; MasPar time 237.34 Seconds 4.382 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-991-628-6 (1-15) from US08991628.pep 109 1 SARTLNNRYTGPYTF 15

Scoring table: PAM 150 Gap 15

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb112

1:sp_archea 2:sp_bacter1a 3:sp_fung1 4:sp_human 5:sp_1nvertebrate 6:sp_mamma1 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 26.282; Variance 35.962; scale 0.731

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	BB	ID	Description	Pred. No.
_	67	61.5	993	=	035902	DESMOGLEIN 3 (FRAGMENT	9.59e-02
2	62	56.9	1187	13	093284	8	9.43e-01
ω	61	56.0		N	024780	CELLODEXTRIN PHOSPHORY	1.47e+00
4	60	55.0	949	10	Q9XE44	PUTATIVE REVERSE TRANS	2.29e+00
5	60	55.0	973	5	081508	T7M24.4 PROTEIN.	2.29e+00
σ	59	54.1	163	N	053240	HYPOTHETICAL 18.2 KD P	3.53e+00
7	59	54.1	330	_	059397	330AA LONG HYPOTHETICA	3.53e+00
60	59	54.1	360	N	Q50378	FERRIC EXOCHELIN BIOSY	3.53e+00
9	59	54.1	531	N	066695	HYPOTHETICAL 62.8 KD P	3.53e+00
10	83	53.2	211	14	201124	COAT PROTEIN VP1 (FRAG	5.43e+00
11	58	53.2	332	,_	029749	CTASE	5.43e+00
12	58	53.2	506	տ	Q17381		5.43e+00
13	58	53.2	770	14	Q07117	HYPOTHETICAL 87.2 KD P	5.43e+00
14	57	52.3	08	14	Q76025	ENVELOPE GLYCOPROTEIN	8.32e+00
15	57	52.3	175	w	Q05776	SIMILAR TO MSF1 PROTEI	8.32e+00
16	57	52.3	449	v	Q19076	CODED FOR BY C. ELEGAN	8.32e+00
17	57	52.3	772	u	060958	CCP.	8.32e+00
18	56	51.4	90	4	000353	INTEGRASE (FRAGMENT).	1.27e+01
19	56	51.4	90	4	000349	INTEGRASE (FRAGMENT).	1.27e+01
20	56	51.4	114	4	Q9Y641	POL PROTEIN (FRAGMENT)	1.27e+01

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22
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P70355	Q9YK99	Q9WHV7	Q44488	087985	Q61918	026886	056251	Q9WHJ6	Q61523	Q9WJC9	Q9WJC8	Q9Y141	074872	082468	Q9XI94	Q86500	Q26638	P70248	Q9Z0R7	Q80873	Q80875	060051	002474
GAG-POL POLYPROTEIN.	POL POLYPEPTIDE (FRAGM	POLYMERASE (FRAGMENT).	NIFEN2.	HYPOTHETICAL 98.1 KD P	POL PROTEIN (FRAGMENT)	CONSERVED PROTEIN.	29 KDA PROTEIN.	REVERSE TRANSCRIPTASE.	POLYMERASE POLYPROTEIN	NONSTRUCTURAL POLYPROT	NONSTRUCTURAL POLYPROT	BCDNA.GH05741.	HYPOTHETICAL 52.6 KD P	_	F7A19.1 PROTEIN.	M33 RNA FOR A NONSTRUC	2 ALPHA FIBRILLAR COLL	MYOSIN IF.	PUTATIVE TASTE RECEPTO	HYPOTHETICAL 87.3 KD P	HYPOTHETICAL 74.0 KD P	ALPHA-AMYLASE PRECURSO	PUTATIVE RNA-DIRECTED
	2.89e+01	:-	2.89e+01	2.89e+01			2.89e+01	2.89e+01	2.89e+01	1.92e+01	1.92e+01	1.92e+01	1.92e+01	1.92e+01	1.92e+01	1.27e+01	1.27e+01	1.27e-01	1.27e+01	1.27e+01	1.27e+01	1.27e+01	1.27e+01

ALIGNMENTS

RESULT 2 ID 093284 PRELIMINARY; PRT; 1187 AA. AC 093284; DT 01-NOV-1998 (TREMBLrel. 08, Created) DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update) DT 01-MAY-1999 (TREMBLREL. 10, Last annotation update) DE POL POLYPROTEIN (FRAGMENT). GN POL. OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;	Query Match 61.5%; Score 67; DB 11; Length 993; Best Local Similarity 66.7%; Pred. No. 9.59e-02; Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1; Db 512 SYRTLDRGKYTGPYT 526		RESULT 1 1 O35902 AC O35902; AT O1-JAN-1998 (TEMBLrel. 05, Created) DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update) DT 01-VAN-1998 (TEMBLrel. 12, Last annotation update) DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update) DE DESMOGLEIN 3 (FRAGMENT). GN DSG3. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Best Local s
Matches
                                SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
LIN X., KAUL S., SHEA T.P., FUJII O
BARNSTEAD M.E., MASON T.M., BOWMAN
CARRERA A.J., CREASY T.H., BUELL C.
FRASER C.M., VENTER J.C.;
"AIBDIOOPSIS thaliana chromosome II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U1-NOV-1999 (TrEMBLrel. 12, Cre
01-NOV-1999 (TrEMBLrel. 12, Las
01-NOV-1999 (TrEMBLrel. 12, Las
PUTATIVE REVERSE TRANSCRIPTASE.
T5M2.2.
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Q9XE44;
Q1-NOV-1999
Q1-NOV-1999
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MEDLINE: 98382517.
POULTER R.T.M., BUTLER N
"A retrotransposon famil
Gene 215:241-249(1998).
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024780;
01-JAN-1998
01-JAN-1998
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC27405;
KAWAGUCHI T., IKEUCHI Y., TSUTSUMI N.
J. Ferment. Bloeng. 85:144-149(1998).
EMBL; AB006822; BAA22081.1; -.
SEQUENCE 980 AA; 111183 MW; ABBAE
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Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu
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Similarity 60.0%;
9; Conservative
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Firmicutes; Bacillus/Clostridium
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8 (TrEMBLrel. 05,
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IN PHOSPHORYLASE.
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                                                                                                     , FUJII C.Y., SHEN M., BOWMAN C.L., RONNING BUELL C.R., TOWN C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence up
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SOME II BAC T5M2 .
EMBL/GenBank/DDBJ
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9.43e-01
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                                                                                                     , VANAKEN S.E.,
G C.M., BENITO M.
,, NIERMAN W.C.,
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Best Local &
Matches
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WATERSTON R.;
Submitted (JUL-1998) to the Elevantic AF077408; AAC26251.1; -
PEAM; PF00078; rvt; 1.
PFOMENCE 973 AA; 112369 M
STRAIN-H37RV;
OLIVER K., HARRIS D.;
Submitted (JAN-1998)
[2]
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081508;
01-NOV-1998
01-NOV-1998
01-MAY-1999
17M24.4 PROT
                                                                                                                Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Corynebacterineae; My
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                 HYPOTHETICAL 18.2 KD MTV012.05.
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01-JUN-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
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STRAIN-CV. COLUMBIA;
STRAIN-CV. LANGSTON Y., STONEKING T., DRONE K.,
"The sequence of Arabidopsis thaliana T7M14.";
"The sequence of the EMBL/GenBank/DDBJ de
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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RNA-directed DNA polymerase
SEQUENCE 949 AA; 108395
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MEDLINE; 96181548.
PHILIPP W.J., POULET :
BALASUBRAMANIAN V., H
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EMBL; AP000007; BAA30834.1; --
PFAM; PF01118; Semialdhyde_dh; 1.
SEQUENCE 330 AA; 37168 MM; D80618ED C
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STRAIN-H37RV;
BARRELL B.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIKUCHI H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
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Archaea; Euryarchaeota;
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EMBL: AL021287; CAA16076.
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BLOOM B.R.,
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DE HYPOTHETICAL
GN AQ_372
OS AQUIFEX BEOLI
OC BACTETIA: AQQ
RP SEQUENCE FROM
RN [1]
RP SEQUENCE FROM
RN ELLMAN D.E.,
RA FELDMAN R.A.
RA FELDMAN R.A.
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RA GRAHAM D.E.
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RA SEQUENCE FROM
RC STRAIN-VF5;
RL SUBMITTED (JU
DR PELDMAN R.A.
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Q01124
Q01124;
Q01-124;
Q1-NOV-1996
Q1-NOV-1998
COAT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-VF5;
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LEN GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AE000686; AAC06652.1; -
Hypothetical protein.
Hypothetical protein.
SEQUENCE 531 AA; 62830 MW; 585EBE7E CRC32;
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DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX GRAHAM D.E., OVERBEER R., SNEAD M.A., KELLER M., AUJAY M., FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquaeolicus.";
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Aquifex aeolicus.
Bacteria; Aquificales;
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EMBL; U10425; AAC43261.1; -.

HSSP; P23882; IFMT.

PFAM: PFOS51; formyl_transf; 1.

SEQUENCE 360 AA; 41130 MW; A81D7F3B CRC32;
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Similarity 38.5%;
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larity 66.7%;
Conservative
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Pred. No.
1; Misma
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Pred. No. 3.
5; Mismatc
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RESULT 11

ID 029749
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DE NITRATE REDUC
GN AFCSO1.
OS Archaeeglobus
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RN (2)
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RX MEDLINE; 9804
RA KLENK H.-P.
RA KETCHUM K.A.,
RA KIRKNESS E.F.
RA PETERSON S.,
RA COTTON M.D.,
RA COTTON M.D.,
RA COTTON M.D.,
RA COTTON M.D.,
RA SADOW P. W., (
RA VENTER J.C.;
RT "The Complet,
RT reducing arc;
Nature 390:3
DR TIGR: AF0501
DR TIGR: AF0501
KW Hypothetical
SQ SEQUENCE 3
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NON_TER
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DOMAIN
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SEQUENCE
211
                                                                                                                                         "The complete genome sequence of reducing archaeon Archaeoglobus Nature 390:364-370(1997).
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Aphthovirus
[1]
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EMBL: M90377: AAA91495.1;
PFAM: PF00073; rhv: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaeoglobus fulgidus.
Archaea: Euryarchaeota:
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MARTINEZ M.A., DOF
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ARTINEZ M.A., DOPAZO J., HERNANDEZ J., MATEU M.G., SUBRA-
DOMINGO E., KNOWLES N.J.;

"Evolution of the capsid protein genes of foot-and-mouth
"Evolution of wariation without accumulation of amino
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                                                                                                                         AE001069; AAB90736.1;
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Similarity 53.8%;
7; Conservative
                       Similarity
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211 AA;
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332 AA; 3
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(TIEMBLrel. 05, Last sequence update)
(TIEMBLrel. 07, Last annotation update)
UCTASE, GAMMA SUBUNIT, PUTATIVE.
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4; Mismatc
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fulgidus.";
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5,43e+00;
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SIMILARITY).
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OF PROTEINS VP1, VP2
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01-NOV-1996
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RTLNNRYTGPYT
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SEQUENCE FROM N.A.
MEDLINE; 90066400.
KOZLOV YU.V., FRANAS'EV B.N., R
KULAEVA O.I., DOLYA V.V., ATABE
"Primary structure of RNA 3 of
Variability.";
Mol. Biol. (Mosk) 23:1080-1090(
                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Crea
01-NOV-1996 (TrEMBLrel. 01, Last
01-NOV-1998 (TrEMBLrel. 08, Last
HYPOTHETICAL 87.2 KD PROTEIN
Barley stripe mosaic vitus (BSMV
Viruses; SSRNA positive-strand v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MORTIMORE B.;
Submitted (JAN-1998) to the EMBL; U51163; AAA96319.1; -
EMBL; 292833; CAB07378.1; -
HSSP; Q63245; 2HFH.
                                                                                 Hypothetical protein. SEQUENCE 770 AA; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00657; FORK_HEAD_1; PROSITE; PS00658; FORK_HEAD_2; PFAM; PF00250; FORK_head; 1. PRINTS; PR0053; FORKHEAD. SEQUENCE 506 AA; 55426 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditi
720 KALVNRYRSPYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                      Biol. (Mosk) 23:1080-1090(1989).
X52774; CAA36983.1; -.
PF00978; RNA_dep_RNApol2; 1.
                                           Similarity
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                                                                                 87176 MW;
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1; ·
                                                                                                                                                           B.N., RUPASOV V.V.,
ATABEKOV I.G., BAEV
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Pred. No. 5.43e+00
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EMBL/GenBank/DDBJ
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RC STRAIN-$288C (AB972);

RX MEDLINE; 97313267.

RX MEDLINE; 97313267.

RA JOHNSTON M., HILLIER L., RILES L., ALBERWANN K., ANDRE B., ANSORGE W.,

RA JOHNSTON M., HILLIER L., DUBJOIS E., DUSTERNOFT A.,

RA LOUIS C., BRUCKNER M., GOFFEAU A., HEBLING U., HEUMANN K.,

RA HEUSS-NEITZEL D., HILBERT H., HILGER F., KLEINE K., KOTTER P.,

RA HOUSS-NEITZEL D., HILBERT H., HILGER F., KLEINE K., KOTTER P.,

RA HOUSS E.J., MESSENCHY F., MEWES H. W., MIOSGA T., MOSTL D.,

RA MULLER AUBER S., NENTWICH U., OBERMAIER B., PIRAVANDI E., POHL T.M.,

RA PORTETELLE D., PURNELLE B., RECHMANN S., RIEGER M., RINKE M., ROSE M.,

RA PORTETELLE D., PURNELLE B., SCHHALRE P., SCHWARER S.,

RA GHARFE M., SCHERENS B., SCHOLLER P., SCHWAGER C., SCHWARZ S.,

RA VIERENDEELS F., VOET M., VOLCKAERT G., VOSS H., WANBUTT R., WEDLER E.,

RA VIERENDEELS F., VOET M., VOLCKAERT G., VOSS H., WANBUTT R., WEDLER E.,

RA WEDLER H., ZIMMERMANN F.K., ZOLLNER A., HANI J., HOHEISEL J.D.;

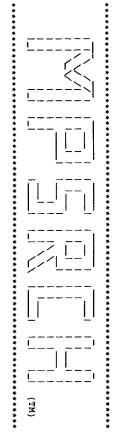
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
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Best Local :
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Q05776; PRELIMINARY;
Q05776; O1-NOV-1996 (TIEMBLIFEL 01, C:
Q1-NOV-1996 (TIEMBLIFEL 08, L:
Q1-NOV-1998 (TIEMBLIFEL 08, L:
SIMILAR TO MSF1 PROTEIN.
                                                                                                                                                                                                                 SEQUENCE FROM STRAIN-S288C (
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17
076025
PRELIMINARY; PRT; 80 AA.
076025;
01-NOV-1996 (TIEMBLIEL 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-MAY-1999 (TIEMBLIEL 10, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
SEQUENCE FROM N.A. STRAIN-S288C (AB972); WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Diversity of V3 region sequences of human immunodeficiency viruses type 1 from the central African Republic."; AIDS Res. Hum. Retroviruses 9:997-1006(1993). EMBL; L11498; AAC37829.1; -...
PFAM: PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                     Nature 387:0-0(0).
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MEDLINE; 94107601.
MURPHY E., KORBER B.T., GEORGES-COURBOT M.C., YOU B., PINTER A.,
COOK D., KIENY M.P., GEORGES A., MATHIOT C., BARRE-SINOUSSI F.,
                                                                                                                                                                        Submitted (SEP-1994) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Envelope protein.
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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Pred. No. 8.32e+00;
2; Mismatches 1;
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STRAIN-S288C (AB972);
CHERRY J.M.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U14913; AAB67434.1; -.
SEQUENCE 175 AA; 20108 MW; 9FCA0042 CRC32;
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                        19 SRAFFNRYPNPYS 31
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Search completed: Sat May 13 07:28:45 2000 Job time: 251 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 07:37:01 2000; MasPar time 3.01 Seconds 118.060 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-991-628-7 (1-15) from US08991628.pep

OSGTMRTRHSTGGTN 15

Scoring table: PAM 150 Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 17.183; Variance 54.742; scale 0.314

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222211111111 2222111111111111111111111	Result
0.05	Score
100.0 54.00.0 100.	Query Match
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R R R R R R R R R R R R R R R R R R R	ID
Self epitope of desmog Human pemphigus vulgar viral haemagglutinin n Nod L gene product. Topoisomerase II bindi Cold accilmatization p CIITA (Class II transa clivat A. nidulans phosphenol CIITA (Class II transactivato Class II transa activat CIITA (Class II transa Bacillus licheniformis Alpha amylase H1337/NI Alpha amylase H1337/TI Alpha-amylase V128E/HI Alpha-amylase V128E/HI M15V alpha-amylase. Bacillus licheniformis	Description
5.70e-04 6.17e-01 1.99e+02 1.99e+02 2.51e+02 2.51e+02 2.51e+02 2.51e+02 2.51e+02 2.51e+02 2.51e+02 3.16e+02	Pred. No.

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PelB signal-Termamyl-l	B. licheniformis acid	Alpha-amylase protein.		-amylase	An alpha-amylase (Am-L	Bacillus licheniformis	A4 form alpha-amylase	B.licheniformis mutant	Alpha-amylase N104D/H1	M197F alpha-amylase.	M15A alpha-amylase.	M15N alpha-amylase.	M15K alpha-amylase.	M15D alpha-amylase.	Alpha-amylase protein	Alpha-amylase mutant M	Alpha-amylase mutant M	M15E alpha-amylase.	M197T alpha-amylase.	M15H alpha-amylase.	M197P alpha-amylase.
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ALIGNMENTS

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ilarit Cons	W04847 standard; pepti W04847 standard; pepti W04847 standard; pepti 18-FEB-1997 (first en Self epitope of desmog Tolarisation; self-epi autoantigen; HLA; huma pemphigus vulgaris; de herpes simplex virus; human papillomavirus; influenza; haemaggluti HOMO Sapiens. W09627387-A1. 12-SEP-1996; U03182. 07-MAR-1995; U5-400796 (HARD) HARVARD COLLEG Strominger JL, Wucher WPI; 96-4251842. Wucher WPI; 96-4251842. Wucher Strominger JL, Wucher WHI; 96-4251842. Wucher WPI; 96-42518142. Wucher WPI; 96-42518142. Wucher WPI; 96-42518142. Wucher Strominger JL, Wucher WPI; 96-42518142. Wucher WPI; 96-42518142. Wucher WIG As autoantifeation of othe auto-immune disease Claim 1; Page 42; 58pp Pharmaceutical preparaeither an isolated hum (MBP) polypeptide which autoantiden; or an isolated hum (MBP) polypeptide which colerising an individuals sequence corresponding protein, such as HLA-D disease and which bind T-cells in individuals derived from the human and is implicated as a derived from the human sequence 15 AA;
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DB 1; L 5.70e-04; tches 0	de; 15 AA. Implicated in autoimmune clope; antigen; autoimmune disease leukocyte antigen; T-cell; thym moglein; multiple sclerosis; pdenovirus; multiple sclerosis; pstein-Barr virus; DNA polymeras; pstein-Barr virus; DNA polymeras; in; reovirus; sigma protein. English. English. English. English. Ions for tolerisation to antigen in non-collagen or non-myslin bas; is capable of tolerising an ind to that polypeptide. In both all to that polypeptide in cludes an amin, to a sequence motif for a MHC cl, which is associated with a hum, to the polypeptide to activate with the autoimmune disease. Thi desmoglein 3 protein (amino acid self epitope in pemphigus vulgar desmoglein protein are described
eng;	utoimmune ine disease cell; thym rosis; obtain. The contrast contain. The contrast in the cont
Length 15; ; 0; Indels	de; 15 AA. Iein 3, implicated in autoimmune disease. cope; antigen; autoimmune disease; cope; antigen; autoimmune disease; cope; antigen; autoimmune disease; cope; antigen; autoimmune disease; cope; antigen; autoimmune disease; pstein: Barr virus; DNA polymerase; cope; antigens and multiple sclerosis non-self clease treatment, and method for cope; self and non-self antigens implicated in cope; self and non-self antigens implicated in cope; self and non-self antigens implicated in cope; self and non-self antigens implicated in cope; self and non-self antigens and individual to cope; self antigens or non-myslin basic protein cope; self antigens and individual to cope; self antigens and individual to cope; self or non-self) includes an amino acid to a sequence motif for a MHC class II to the polypeptide to activate autoreacti with the autoimmune disease. This peptide desmoglein 3 protein are described in w04841
0;	non-self non-self compris c protei vidual t vidual t vasesie o asesie o ase
Gaps	W04847; standard; peptide; 15 AA. W04847; standard; peptide; 15 AA. W04847; standard; peptide; 15 AA. W04847; standard; peptide; 3, implicated in autoimmune disease. Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris; desmoglein; multiple sclerosis; herpes simplex virus; adenovirus; phosphomannomutase; human papillomavirus; bestein-Barr virus; DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein. W0567387-A1. 12-SEP-1996. (HARD) HARVARD COLLEGE. Strominger JL, Wucherpfennig KW; WPI; 96-425218/42. 07-MAR-1995; US-400796. (HARD) HARVARD COLLEGE. Strominger JL, Wucherpfennig KW; WPI; 96-425218/42. 19-42-19-19-19-19-19-19-19-19-19-19-19-19-19-
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R10423 standard; Protein; 140
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Nod L gene product.
Nod genes; parasite; toxin; p
Bradyrhizobium japonicum.
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09-DEC-1988; JP-311655.
(JAPG ) NIPPON ZEON KK.
WPI; 90-228484/30.
N-PSDB; Q05319.
Recombinant vaccinia virus -
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US7798918-A.

15-DEC-1992.

27-NOV-1991; 798918.

27-NOV-1991; US-798918.

(USSH) US DEPT HEALTH & I

Amagai M, Klaus-kovtun V

WPI; 93-067436/08.

N-PSDB; Q35992.
                                                                                                                                                                                                                                                                                                                                                            membrane fusion protein in combined to genom region. Disclosure; p; Japanese. Fragment of parainfluenza viral membrane fusion protein may be incorporated into the vaccina virus, which may the as a live vaccine for cows.
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Bovine parainfluenza type III virus.
702156883-A.
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This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosts and treatment of pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human pemphigus vulgaris 130kD antigen.
Pemphigus vulgaris; skin disease; autoantibodies;
keratinocyte cell surface antigen; glycoprotein;
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Disclosure; Page 4; llpp; English.
The nod L gene product may be used to nod- mutants of Bradyrhizobium or enhance nodulating ability.
Sequence 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agent
Claim 2; Page 13-14; 28pp; Japanese.
Claim 2; Page 13-14; 28pp; Japanese.
This sequence represents the topolsomerase II binding protein (TopBP)
the invention. The TopBP protein is useful as an anticancer agent. Top
can be used as the target molecule for anticancer agent.
Sequence 392 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-1997; 251544.
17-SEP-1997; JP-251544.
(CHUS) CHUGAI PHARM CO
(TSUR/) TSURUO T.
WPI; 99-257704/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            703182 standard; 1
Y03182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Topoisomerase
Topoisomerase
Homo sapiens.
              04-AUG-1994.
21-JAN-1994; U00581.
21-JAN-1993; US-007107.
(UYFL) UNIV FLORIDA.
Guy CL,
                                                                                                                                      Cold acclimatization protein CAP160 from spinach leaf. Cold acclimatization; cold-tolerance; transgenic plant; drought-resistance; drought-tolerance; crop improvement freezing-tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (STAC/) STACEY G. Stacey G. Schell MG, Nieuwkoop WPI: 91-036225/05.
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08-JAN-1991.
24-JUL-1987;
24-JUL-1987;
                                                                                                    Spinacia ole
W09417186-A.
                                                                                                                                                                                                                                                       T 6
R56550 standard;
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                                                                                                                                                                                                                                            R56550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Topoisomerase II-
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5 MRTRHSIGG 13
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  NIV FLORIDA.
Haskell DW,
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llarity 66.7%;
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e II binding protein;
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US-077561.
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Pred. No. 1.99e+02
1; Mismatches
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Pred.
5; M
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d. No. 1.99e+02;
Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding MHC class II trans-activator polypeptide(s) - useful re.g. as primers for enzymatic amplification, as detection probes or as inhibitors of expression of genes encoding MHC in dendritic cells in disclosure; pages 66-99; 86pp; French.

The present sequence represents type IV CIITA (class II transactivator) protein. The products can be used to treat diseases for which enhanced expression of genes coding for MHC class II molecules is desired, especially where the enhanced expression is desired in dendritic cells or after induction by a cytokine, especially interferon-gamma or interleukin-4. Inhibitors of the gene or protein coding for MHC class II molecules is coding for MHC class II molecules is desired or ancer treatment.

Sequence 830 AA;
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Best Local S
Matches
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Best Local Similarity
Matches 5; Conse
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EP-874049-A1.
28-OCT-1998.
21-APR-1998: 400968.
22-APR-1997; FR-004954.
(TRGE) TRANSGENE SA.
                                                                                                                                                                                                                                                                                                                W57057 standa
W57057;
W57057;
17-AUG-1998
                                                                                                                                                      Class II trans activator (CIITA) 151 deletion mutant. Class II trans activator; MEC, CIITA, autoimmune disease; tree transplantation; xenograft; major histocompatibility complex; gene therapy; arthritis; ribozyme; 151 deletion mutant.
                                                                                                                gene therapy;
Homo sapiens.
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Claim 6; Page 29; 49pp; English.
Claim 6; Page 29; 49pp; English.
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Cold acclimatisation proteins CAP85 and CAP160 and their nucleotide sequences - used to confer increased cold tola and drought resistance on plants and microorganisms by go
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WPI; 98-559115/48.
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01-FEB-1999
    M1sc_d1fference
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Similarity 53.3%;
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larity 55.6%;
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4; Mismatc
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Pred. No. 2.51e+02;
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nce and/or drought-re
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2.51e+02;
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PT rejection

Colaim 15; Pages 69-72; 104pp; English.

CC Claim 15; Pages 69-72; 104pp; English.

CC Claim 15; Pages 69-72; 104pp; English.

CC Claim 15; Pages 69-72; 104pp; English.

CC (CIITA) polypeptide. The N-terminal region of the wild type CIITA is

CC (CIITA) polypeptide. The N-terminal region of major

CC (CIITA) polypeptide. The N-terminal region of major

CC histocompatibility complex (MIC) class I antigens. A ribozyme targeted

CC obases 1159-1161 (GUA) of human CIITA mRNA, or corresponding target in

CC other species and the CIITA polypeptide can be used to reduce expression

CC disease (e.g. arthritis and diabetes) or to treatment of autoimmune

CC disease (e.g. arthritis and diabetes) or to treat non-human animals

CC intended as source of xenografts. The ribozyme and the CIITA polypeptide

CC may be generated in vivo by gene therapy, using the encoding nucleic

CC acids targeted for localised suppression of the immune response. Material

CC transfected with the CIITA encoding nucleic acids are used for animal-to-

CC class II antigens, in cells that express them constitutively or after

CC class II antigens, in cells that express them constitutively or after

CC competitively inhibits endogenous CIITA.

CC competitively inhibits endogenous CIITA.
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Matches
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16-APR-1998.
08-OCT-1997; G02751.
21-MAR-1996; GB-005911.
08-OCT-1996; GB-020940.
(CHIL-) INST CHILD HEALTH.
                                                                                                                                                                                                                                            24-AUG-1984; 177352.
24-AUG-1984; JP-177352.
(KOHZ/) KOHZUKI H.
WPI; 86-115948/18.
bacteria.

Disclosure: Fig 1: 16pp; Japanese.
Transforming a bacteria with the PPC encoding some states of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the 
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PPC gene of cloned photosynthetic intensifying photosynthesis carbon
                                                                                                                                                                                                                                                                                                                                                                              PPC; photosynthesis; Anacystis nidulans. J61056082-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   03-SEP-1991 (first entry)
A.nidulans phosphenol pyru
PPC; photosynthesis; pA181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deleted form of the class II trans-activator that reduces class II antigen expression - and ribozyme directed to trans-activator mRNA, related nucleic acid, vectors, transformed cells and antibodies, used for treating auto-immune disease and to inhibit xeno-graft
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pA181; pA171; pA172; pA172A.
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Pred. No. 2.51e+02;
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01-FEB-1999
CIITA (class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents type II CIITA (class II transactivator) protein. The products can be used to treat diseases for which enhanced expression of genes coding for MHC class II molecules is desired, especially where the enhanced expression is desired in dendritic cells or after induction by a cytokine, especially interferon-gamma or interleukin-4. Inhibitors of the gene or protein can be used to treat diseases for which reduced expression of genes coding for MHC class II molecules is desired or can be used as vaccines, especially for cancer treatment.
                                                                                    binding_site
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21-APR-1998; 400968.
22-APR-1997; FR-004954.
(TRGE) TRANSGENE SA.
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19-APR-1995
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5; Conservative
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II transactivator) type II protein.
class II transactivator; MHC class II molecule;
gamma; interleukin-4; vaccine; cancer treatment.
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For Gene encoding a protein displaying class II trans-activator

FT Gene encoding a protein in compan. for treating diseases associated

FT with impaired expression of MHC-II genes, etc.

FX Claim II; Page 17-21; 32pp; English.

CC This protein sequence is encoded by the gene represented in Q88110.

CC This protein is a class II gene expression in Blymphocytes. The DNA

CC control of MHC class II gene expression in Blymphocytes. The DNA

CC sequence has two in frame start codons. The first of these is at position

CC sequence has two in frame start codons. The first of these is at position

CC sequence has two in frame start codons and the second is present

CC and acts as the translation initiation site. The second is present

CC contains three stretches rich in proline/serine/threonine. It also

CC contains a region rich in glutamate/aspartate (an acidic region) and an

CC ATP/GTP binding cassette. The acidic regions followed by three stretches

CC rich in proline, serine and threonine resembles a transcription

CC acids 979 to 1061 that shows weak homology with the N terminal portion of

CC acids 979 to 1061 that shows weak homology with the N terminal portion of

CC sequence can be used to treat diseases where a decrease in the level of

CC expression of MHC cells II genes is desired e.g. insulin dependant

CC diabetes, multiple sclerosis, lupus erythematosis and rheumatoid

CC contains.

CC contains and the level of

CC contains and the level of

CC contains and the level of

CC contains and the level of

CC contains and the level of

CC arthritis.
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Best Local Similarity
Matches 5; Conse
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22-AUG-1995; U10691.
24-AUG-1994; US-295502.
(HARD) HAKVARD COLLEGE.
Douhan J, Glimcher LH,
WPI; 96-151325/15.
N-PSDB; T18028.

N-PSDB; T18028.

N-PSDB; T18028.

N-PSDB; T18028.

Nethods which inhibit transcription activation by CIITA - causes inhibition of MHC class II gene expression, used in therapy of auto:immune disorders

Example 1; Page 36-41; 64pp; English.

A genomic DNA sequence (T18028) codes for the class II transactivator. CIITA (R81569), a protein essential for activation of transcription of MHC class II genes. The CIITA transcription activation domain provides useful information for identifying cpds. which inhibit CIITA-dependent transcription. Such cpds. are potential autoimmune disease therapeutics by virtue of their ability to inhibit transcription of the MHC class II genes. A second portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class II transactivator. CIITA; class II transactivator; major histocompatibility comple
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N-PSDB; Q88110.
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26-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                domain
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llarity 55.6%;
Conservative
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301. .1
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                                                                                                                                                                                                                                                                                                                                                                                         "interaction domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ivator; transcription; MHC;
complex class II; autoimmune disease;
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Pred. No. 2.51e+02;
4; Mismatches 0;
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                                                                                                                                                                      This represents a class II trans activator (CIITA) polypeptide. When the N-terminal region of the CIITA is deleted, it can be used for reducing the expression of major histocompatibility complex (MHC) class II antigens. A ribozyme targeted to bases 1159-1161 (GUA) of human CIITA mRNA, or corresponding target in other species and the CIITA polypeptide can be used to reduce expression of MHC class II antigens, particularly for treatment of autoimmune disease (e.g. arthritis and diabetes) or to treat non-human animals intended as source of kenografts. The ribozyme and the CIITA polypeptide may be generated in vivo by gene therapy, using the encoding nucleic acids targeted for localised suppression of the immune response. Material from transgenic animals in which at least some cells are stably transfected with the CIITA encoding nucleic acids are used for animal-to-human transplantation. The CIITA polypeptide suppresses synthesis of class II antigens, in cells that express them constitutively our after lymphokine induction. It has no transcription activity but still binds to regulatory proteins in the promoter region of class II genes, so competitively inhibits endogenous CIITA.
                                                         Query Match
Best Local S
Matches
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Best Local
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08-OCT-1997; G02751.
21-MAR-1997; GB-005911.
08-OCT-1996; GB-020940.
(CHIL-) INST CHILD HEALTH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deleted form of the class II trans-activator that reduces class II antigen expression - and ribozyme directed to trans-activator mRNA, related nucleic acid, vectors, transformed cells and antibodies, used for treating auto-immune disease and to inhibit xeno-graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class II trans activator (CIITA) polypeptide.
Class II trans activator; MHC; CIITA; autoimmune disease; treatment;
transplantation; xenograf; major histocompatibility complex; diabetes;
gene therapy; arthritis; ribozyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; V28716
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W57056 standard: Protein; 1130 AA.
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163 . 195
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Pred. No. 2.51e+02;
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PI Mach B;

DR WP; 98-559115/48.

PT DNA encoding MHC class II trans-activator polypeptide(s) - useful PT e.g. as primers for enzymatic amplification, as detection probes or as inhibitors of expression of genes encoding MHC in dendritic cells CC The present sequence represents a type I CIITA (class II transactivator) CC protein. The products can be used to treat diseases for which CC enhanced expression of genes coding for MHC class II molecules is CC desired, especially where the enhanced expression is desired in CC dendritic cells or after induction by a cytokine, especially CC interferon-gamma or interleukin-4. Inhibitors of the gene or protein CC can be used to treat diseases for which reduced expression of genes CC coding for MHC class II molecules is desired or can be used as vaccines, coding for Class II molecules is desired or can be used as vaccines,
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Best Local
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The present sequence represents type III CITA (class II transactivator) protein. The products can be used to treat diseases for which enhanced expression of genes coding for MHC class II molecules is desired, especially where the enhanced expression is desired in dendritic cells or after induction by a cytokine, especially interferon-gamma or interleukin-4. Inhibitors of the gene or protein can be used to treat diseases for which reduced expression of genes coding for MHC class II molecules is desired or can be used as vaccines, especially for cancer treatment.
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22-APR-1997; FR-004954.
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CIITA (class II transactivator) type I protein.
CIITA gene; class II transactivator; MHC class II molecule;
interferon-gamma; interleukin-4; vaccine; cancer treatment.
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CIITA gene; class II transactivator; MHC class II molecule;
interferon-gamma; interleukin-4; vaccine; cancer treatment.
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21-APR-1998; 400968.
22-APR-1997; FR-004954.
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Query Match

48.58;

Score

48; DB 1;

Length 1207

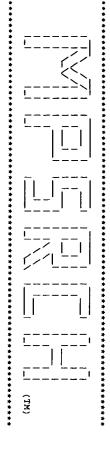
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Best Local Similarity 55.6%; Pred. No. 2.51e*02;

bb 874 (PETIANRO 882)

Oy 1 OSCTNETEN: 9

Search completed: Sat May 13 07:37:08 2000

JOB time: 7 secs.
```



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Sat May 13 07:36:34 2000; MasPar time 4.29 Seconds 164.848 Million cell updates/sec

Description: Perfect Score: >US-08-991-628-7 (1-15) from US08991628.pep 99

1 OSGIMRIRHSIGGIN 15

Tabular output not generated.

Scoring table: PAM 150 Gap 15

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 23.943; Variance 29.203; scale 0.820

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22 23 23	11 11 11 11 10 10	111 10987654321 2110	Result
0 4 4 4 0 0 0 0 0	50 50 51 51 51 51 51 51 51	57 55 55 55 55 55 55 55 55	Score
		100 5770 572 573 573 573 573 573 573 573 573 573 573	Query Match
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S45306 H72542 A25979 I49712	S04605 S11003 FWSYG2 S10851 T15080 JE0417 HNNZB3	IJHUG3 BVFFSL T08428 S33886 S33886 A44991 S33568 IVH30568 IVH30568 IVH30568 INA3806 INA3806 INA3806	Ħ
notch 3 protein - mou hypothetical protein hypothetical 15.9K pr H-2K-s - mouse	glycinin G3 - soybean glycinin G3 precursor glycinin chain Alabx glycinin G1 precursor hypothetical protein aminoglycoside N-acet hemagalutinin neurami	desmoglein 3 precurso sol protein, large sp gene small optic lobe DNA-directed RNA poly protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina protein-tyrosine kina gene m3 protein - Lac kinesin-73 - fruit fl p-Aminobenzoic acid s	Description
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terminal protein prec	nucleocapsid protein	exo-alpha-sialidase (extracellular nucleas	invasion-inducing pro	coatomer complex alph	MHC class II transact	phytochrome A - Popul	phosphoenolpyruvate c	cell division control		nitrate reductase (EC	protein-serine/threon	hypothetical protein	exo-alpha-sialidase (bindin fertilization	transcription factor	scytalone dehydratase	hypothetical protein	probable GTPase-activ	H-2K-sml - mouse	MHC class I histocomp
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ALIGNMENTS

Query Match Best Local Sim: Matches 15;	SUMMARY	937-966 110,180,545	640-999 910-938	496-598 616-639	270-383 390-495	52-157 160-267	50~615	50-999	1-23	FEATURE	A DE TACKED	CLASSIFICATION	#map_position	##Cross-re	#GGCG #GGCG	##Cross-re	##residues	8	#cross-refere	!	#title	#authors	REFERENCE	ACCESSIONS	DATE	ALTERNATE_NAMES	TITLE	RESULT 1
100.0%; Score 99; DB 1; Length 999; Similarity 100.0%; Pred. No. 9.45e-12; 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	#length 999 #molecular-weight 107502 #checksum 8311	#domain desmoylein repeat #label DG1\ #domain desmoylein repeat #label DG2\ #blinding_site carbohydrate (Asn) (covalent) #status	intracellular #status pro	cadherin repeat homology #label CR5\ transmembrane #status predicted #label	cadherin repeat homology *label cadherin repeat homology *label	cadherin repeat homology #label CR1\ cadherin repeat homology #label CR2\	MAT\ #domain extracellular #status predicted #label EXT\	*product desmoglein homolog *status predicted *label **RON	signal sequ		carcium binding; cerr adnesion; duplication; glycoprotein; transmembrane protein		18q12.1-18q12.2	##Cross-references GDB:134030: OMIM:169615		ferences GB:M76482;	1-999 ##label AMA	##MOLECULE type mRNA		pemphiqus vulgaris, a disease of cell adhesion.	novel entrhelial cadhorin	Amagai, M.; Klaus-Kovtun, V.; Stanley, J.R.	A41088	22-Um-1999 A41088	30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change		desmoglein 3 precursor - human	

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Best Local Similarity 61.5%;
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754-771
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#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:7214-7218
#title Molecular cloning and analysis of small optic lobes, a structural brain gene of Drosophila melanogaster.
#cross-references MUID:91334436
#cross-references
#accession T08
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##cross-references GB:M64084; NID:g2760822; PIDN:AAB95431.1; PID:g158483
The sol (small optic lobes) mutation eliminates certain classes of
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                                 Maleszka, R.; de Couet, H.G.; Miklos, G.L.
Proc. Natl. Acad. Sci. U.S.A. (1998) 95:3731-3736
Data transferability from model organisms to human beings:
insights from the functional genomics of the flightless
region of Drosophila.
nces MUID:98188272
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11-Jun-1999 #sequence_revision 11-Jun-1999
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30-Jun-1992 #sequence_revision 30-Jun-1992
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small optic lobes protein -
translated from GB/EMBL/DDBJ
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#active_site Cys, His, Asn #status predicted
th 1597 #molecular-weight 174713 #checksum 8253
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, large splice form .
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Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                    #authors Kaufmann, J.; Florian, V.; Klein, A.

#journal Nucleic Acids Res. (1992) 20:5995-5999

#title 'TGA cysteine codons and intron sequences in conserved and nonconserved positions are found in macronuclear RNA polymerase genes of Euplotes octocarinatus.

#cross-references MUID:93096587

#accession S70414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Kaufmann, J.; Klein, A.

Nucleic Acids Res. (1992) 20:4445-4450

#title Gene das a possible major determinant for equal

expression levels of genes encoding RNA polymerase subunits
in the hypotrichous ciliate Euplotes octocarinatus.

#cross-references MUID:93027138
                                                                                                                                                                                                                                                 #gene RPB1
#genetic_code SGC9
#introns 30/3; 74/1
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##cross-references EMBL:AF017777; NI
##experimental_source strain Cantons
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##residues 1-1
1 QSGTMRTRHSTGG 13
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                                                                                              h 56.6%;
Similarity 53.8%;
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DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain
RPB1 - Euplotes octocarinatus (SGC9) (fragment)
#formal_name Euplotes octocarinatus
08-Dec-1993 *sequence_revision 10-Nov-1995 *text_change
12-Sep-1997
                                                                                                                                                  DNA binding; nucleotidyltransferase; transcription; zinc finger #length 478 #checksum 3090
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81/2; 290/1; 594/2; 704/1; 1233/3; 1402/3; 1491/3;
#superfamily sol protein; calpain catalytic domain
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                                                                            Conservative
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Pred. No. 3.67e-01;
3; Mismatches 7
                                                                        Score 56; DB 2; L
Pred. No. 6.05e-01;
3; Mismatches 3
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RESULT

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ALTERNATE_NAMES
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Best Local Similarity
                 89-138
149-246
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149-246
266-524
274-282
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*journal New Biol. (1989) 1:66-74

*title Expression of a novel form of

hematopoletic cells.

*cross-references_MUID:91175680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #title A novel Yes-related kinase, Yrk, is e
levels in neural and hematopoietic
#cross-references_MUID:93205395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *journal
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                                                                                                                                                                                                                                                                                          ##molecule_type mRNA
##residues 1-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-534 ##label COO
##cross-references GB:M77265; NID:g309241
##note in the authors' translation an additional residue Leu
##note was shown after Lys, for residue 459

IFICATION #superfamily protein-tyrosine kinase src; protein kinase
homology; SH2 homology
ATP; autophosphorylation; phosphoprotein; phosphotransferase;
tyrosine-specific protein kinase
                                                                                                                                                                                                                                                             **residues 1-348,'I',350-534 **label SUD2 **presidues 1-348,'I',350-534 **presidues 1-348,'I',350-534 **presidues 1-348,'I',350-534 **presidues 1-348,'I',350-534 **presidues 1-348,'I',350-534 **presidues 1-348,'I',350-534 **presidues 1-348,'I',350-534 **presidues 1-348,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-534,'I',350-5
                                                                                                                                                                                                                                                                                                                                                                                                                                               **residues 1-534 **label
**cross-references EMBL:X52841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
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                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, May 1990 \ \mbox{536351}
                                                                                                                    *superfamily protein-tyrosine kinase src; protein kinase
homology; SH2 homology; SH3 homology
ATP; phosphoprotein; phosphotransferase; proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                      Sudol, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J.; Yamamoto, T.
Oncogene (1993) 8:823-831
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protein-tyrosine kinase (EC 2.7.1.112) fyn - chicken
#formal_name Gallus gallus #common_name chicken
31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-tyrosine kinase (EC 2.7.1.112) fyn - mouse
kinase-related transforming protein (fyn)
#formal_name Mus musculus #common_name house mouse
03-Jun-1993 #sequence_revision 30-Sep-1993 #text_change
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S33568
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                                                                                             transforming protein; tyrosine-specific
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#domain SH2 homology #label SH2\
#domain SH2 homology #label KIN\
#tegion protein kinase ATP-binding motif
              #domain SH3
#domain SH2
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57.1%;
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        homology #label
homology #label
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Pred. No. 9.93e-01;
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SH2\
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#authors
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274-282
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                                                                                                                          ##molecule_type DNA

##residues 514-524,'QRS' ##label KAW3

##cross-references GB:M20285; NID:g182844; PIDN:AAA52492.1; PID:g182845

##experimental_source clone pFYN(c)-21; recombinant mutant p57(fyn)
                                                                                                                                                                                                                                                                              ##experimental_source clone pFYN(c)-l1; termination mutant p56(fyn) session 179512
                                                                                                                                                                                                                                                                                                                          ##molecule_type DNA
##residues 514-522 ##label KAW2
##cross-references GB:M20284; NID:g182842; PIDN:AAA52491.1; PID:g182843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-183,'S',185-436,'R',438-537 **label KAW1
##cross-references GB:M14676; NID:9338227; PIDN:AAA36615.1; PID:9
##note the authors translated the codon GAA for residue
Gln and GGA for residue 278 as Gln
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Similarity 57.1%;
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                                                                           Peters, D.J.; McGrew, B.R.; Perron,
Oncogene (1990) 5:1313-1319 In vivo phosphorylation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawakami, T.; Pennington, C.Y.; Robbins, K.C. Mol. Cell. Biol. (1986) 6:4195-4201
Isolation and oncogenic potential of a novel
                                                                                                                 A58826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A25389
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                                                       Laudano,
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novel human

src-like

PID:g338228 sidue 265 as

membrane

association of the

O

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Liptak, L.M.;

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fynB; p59(fyn); protein-tyrosine kinase slk;
                                               TVHUSY #type complete protein-tyrosine kinase (EC 2.7.1.112) fyn,
                                                                                                                                                                                                                                                                                                                                                 #length 534 #molecular-weight 60267 #checksum 4864
                                                                                                                                                                                                                                                                                                                                                                                       *domain protein kinase homology *label KIN\
*region protein kinase ATP-binding motif\
*binding_site ATP (Lys) *status predicted\
*binding_site phosphate (Tyr) (covalent) *status
                                                                                                                                                                                                                                                                                Pred. No. 9.93e-01;
                                                                                                                                                                                                                                                                                                   Score 55;
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                                                 splice form B
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#journal Proc. Natl. Acad. Sci. U.S.A. (19
#title yes-related protooncogene, syn, b
protein-tyrosine kinase family.
#cross-references MUID:86287278 Semba, K.; Nishizawa, M.; Miyajima, N.; Yoshida, M.C Sukegawa, J.; Yamanashi, Y.; Sasaki, M.; Yamamoto, kinase syn; proto-oncogene fyn #formal_name Homo sapiens #common_name man 31-Mar-1988 #sequence_revision 31-Mar-1988 11-Jun-1999 A24314; A25389; I59120; I79512 Sci. U.S.A. (1986) 83:5459-5463 oncogene, syn, belongs to the SEM NID:g181171; PIDN:AAC08285.1; #text_change protein-tyrosine PID:g181172 3.C.;

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FEATURE
89-138
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#authors
#journal
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GENETICS
                                                                   SUMMARY
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#submission submitted to the Brookhaven Protein Data
#cross-references PDB:1NYG
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*cross-references PDB:1SHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #title High-resolution crystal structures of tyrosine kinase domains complexed with proline-rich peptides. #cross-references MUID:95393198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         catalyzes the phosphorylation of a peptidyl tyrosine residue
by ATP
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Crystal structure of the SH3 domain in human Fyn; comparison
of the three-dimensional structures of SH3 domains in
tyrosine kinases and spectrin.
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                                                               #length
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autophosphorylation) #status predicted\
#binding_site phosphate (Tyr) (covalent) #status
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#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
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                                                             #molecular-weight 60762
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*authors Hannig, G.; Ottille, S.; Schartl, M.

*journal Oncogene (1991) 6:361-369

*title Conservation of structure and expression of the

*teross-references MUID:91187435
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*Ittle Structure and expression
*cross-references MUID:90191723
*accession A43806
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#residues 1-537 ##label STE
##cross-references GB:X32188; GB:X52189; NID:g64701;
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#formal_name Xiphophorus helleri
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##cross-references EMBL:AF009630; NID:g3282360; PID:g3282321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTMRTRHSTG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTGTLRTRGGTGVT
JN0578 #type complete p-Aminobenzoic acid synth lividans
                                                                                                                                                                                                                                                                                                                                                                                     T13827 #type complete
kinesin-73 - fruit fly (Drosophila melanogaster)
#formal_name Drosophila melanogaster
20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crutz-Le Coq, A.M.; Cesselin, B.; Commissaire, Kyrlakidis, S.; Chopin, M.C. submitted to the EMBL Data Library, June 1997 Sequence and organization of the lactococcal is phage genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ∄
                                                                                                                                                                                                                                                                                                  Li, H.P.; Liu, Z.M.; Nirenberg, M.
Proc. Natl. Acad. Sci. U.S.A. (1997)
Kinesin-73 in the nervous system of D
T13827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *length 160 *molecular-weight 18072 *checksum 3777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T03369 *type complete
gene m3 protein - Lactococcus phage bIL170
*formal_name Lactococcus phage bIL170
24-Mar-1999 *sequence_revision 24-Mar-1999 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z14903
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                                                                                                                                                 Score 52; DB 2;
Pred. No. 4.24e+00
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 53; DB 2; I
Pred. No. 2.63e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB 2;
Pred. No. 9.93e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                 synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from GB/EMBL/DDBJ
                 OH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lactococcal isometric bIL170
                                                                                                                                                                              Length 1921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 160;
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               4.1.3.-)
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#introns
CLASSIFICATION
SUMMARY
                                    ACCESSIONS
REFERENCE
#authors
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REFERENCE
#authors
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REFERENCE
#authors
#journal
#title
                                                                                                                                                                RESULT
ENTRY
TITLE
ORGANISM
DATE
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ENTRY
TITLE
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##cross-references GB:M64859; NID:g153393; PIDN:AAA26798.1; PID:g153394
COMMENT This enzyme participates in p-aminobenzoic acid biosynthesis.
GENETICS
                                                                                                                                                                                                                                                                                                                                                                                  Ş
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CLASSIFICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.5%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 51.5%;
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Cho, T.J.: Nielsen, N.C.
#journal Nucleic Acids Res. (1989) 17:4388
#title The glycinin Gy(3) gene from soybe
#cross-references MUID:89296500
#accession S04605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Arhin, F.F.; Vining, L.C.
#journal Gene (1993) 126:129-133
#title Organization of the genes encoding p-aminobenzoic
synthetase from Streptomyces 11vidans 1326.
#cross-references_MUID:93231526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                             304 TMRLRHNIGQTS 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 1-481 ##label CHO ##cross-references EMBL:X15123; NID:g18638; ##experimental_source variety Dare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 AGTLRGRPRAGGDD 294
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                                                                                                                                                                                                                                                                                          14
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                                                                                                                                                                                                                                                                                                                                                                                  TMRTRHSTGGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gy3
96/1; 177/3; 352/3
#superfamily glycinin
#length 481 #molecular-weight 54241 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           su4605 #type complete
glycinin G3 - soybean
#formal_name Glycine max #common_name soybean
28-Feb-1990 #sequence_revision 28-Feb-1990 #te
20-Aug-1999
                                                                                                               $11003 *type complete
glycinin G3 precursor - soybean
*formal_name Glycine max *common_name soybean
21-Nov-1993 *sequence_revision 19-Jan-1996 *tr
03-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S04605
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Nielsen, N.C.; Dickinson, Scallon, B.J.; Fischer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Streptomyces lividans
14-Jul-1994 #sequence_revision 14-
22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 2; 1
Pred. No. 6.79e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51; DB 2; I
Pred. No. 6.79e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.
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R.L.;
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Cho, T.J.; Thanh, V.H.; Sims, T.L.; Drews, G.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:CAA33217.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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G. N. ;
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CLASSIFICATION
KEYWORDS
FEATURE
1-19
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CLASSIFICATION
KEYWORDS
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REFERENCE
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ENTRY
TITLE
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SUMMARY
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                                                                                                                                                                                                                             COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.5%;
Best Local Similarity 58.3%;
Matches 7; Conservative
       311-490
107-317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goldberg, R.B.
#journal Plant Cell (1989) 1:313-328
#title Characterization of the glycinin gene family in soybean.
#eross-references MUID:92393391
#accession S11003
                                                                                                                                                                                                                                                                                                                                                                                                   PERENCE $10502

*Bauthors Kitamura, Y.; Arahira, M.; Itoh, Y.; Fukazawa, C.

*Journal Nucleic Acids Res. (1990) 18:4245

*The complete nucleotide sequence of soybean glycinin A2Bla

*title gene spanning to another glycinin gene AlaBlb.

*Cross-references MUID:90332420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors
#journal
#title
                                                                      20-306
                                                                                                                                                                                                                                                                                                                                                                                   #accession
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#accession A23497
                                                                                                                                                                                                                                                                ##molecule_type DNA
481-495 ##label KIT
##residues
481-495 ##label KIT
##residues
From The source of this protein was cotyledon tissue taken 38 days after
                                                                                                                                                                                                                                                                                                                                                              ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          **residues 1-495 **label NEG

**cross-references GB:X02985; NID:gl8614; PIDN:CAA26723.1; PID:gl8615

**experimental_source cv. Bonminori
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##residues 1-484 ##label NIE
##experimental_source variety Dare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##note
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                                                                                                                                                                                                                         flowering.

By homology with the A2Bla component, residues 307-310, and 491-495
                                                                                                                                                                                   processing.
                                                                                                                                                                                                    are removed from the precursor
                                                                                                                                                                                                                                                                                                                                                                                   S10502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Negoro, T.; Momma, T.; Fukazawa, C.
Nucleic Acids Res. (1985) 13:6719-6731
A cDNA clone encoding a glycinin A-la subunit precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FWSYG2 *type complete
glycinin chain AlaBa precursor - soybean
115 globuln; glycinin AlaBlb
#formal_name Glycine max *common_name soybean
31-Mar-1988 *sequence_revision 31-Mar-1988 *text_change
16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gy3
                                                                                                                                       seed; storage protein
                                                                                                                                                          #superfamily glycinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #domain signal sequence #status predicted #label SIG\
#product glycinin G3 #status predicted #label MAT
#length 484 #molecular-weight 54359 #checksum 8616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 because of current nomenclature ambiguities, the authors choose to designate the basic chain as Bx
#product glycinin chain Bx #status predicted #label GLB\
#disulfide_bonds #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the authors translated the codon AAC for residue 449 as
                                                                 #product glycinin chain Ala #status predicted #label SIG
                                                                                                                                                                                                                                                                                                                                                           preliminary; translation not shown
                                                   GE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB 2; Length 484; 
Pred. No. 6.79e+00; 
2; Mismatches 3; Indels
                                                                                                                                                                                                      during posttranslational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                   SUMMARY
                                                                Query Match 51.5%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                   318 TMRLRHNIGQTS 329
 4 TMRTRHSTGGTN 15
                                                                                                                                  #length 495  #molecular-weight 55506  #checksum 8518
                                                              Score 51; DB 1; Length 495; Pred. No. 6.79e+00; 2; Mismatches 3; Indels
                                                                 0
                                                                 Gaps
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Search completed: Sat May 13 07:36:42 2000 Job time : 8 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Sat May 13 07:29:58 2000: MasPar time 89.82 Seconds $5.086 \, \mathrm{Million}$ cell updates/sec

Run on:

Tabular output not generated.

Title: >US-08-991-628-7

Description: (1-15) from US08991628.pep
Perfect Score: 99
Sequence: 1 OSGTMRTRHSTGGTN 15

Scoring table: PAM 150 Gap 15

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 24.519; Variance 27.183; scale 0.902

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	22	2 6	19	18	17	16	15	14	13	12	11	10	9	00	7	6	· Cr	4	w	2		Result	
4 8	4 4	200	4.00	48	49	50	50	50	50	51	51	51	52	55	55	55	55	55	56	57	99	Score	
48.5	80.	л ф л С	80.5	48.5	49.5	50.5	50.5	50.5	50.5	51.5	51.5	51.5	52.5	55.6	55.6	55.6	55.6	55.6	56.6	57.6	100.0	Query	90
510	471	A 55	291	172	230	2318	572	286	120	495	481	475	543	536	536	536	533	533	478	1597	999	Length	
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KR2_VZVD	NRAM TAFPE	COAT_AEDEB	T2EB_HUMAN	SCYD_MAGGR	RL4_MYCLE	NTC3_MOUSE	HEMA_PI3B	AAC8_STRFR	MA5D_SCHJA	GLC1_SOYBN	GLC3_SOYBN	PABB_STRLI	TCPH_HUMAN	FYN_XIPHE	FYN_HUMAN	FYN_XENLA	FYN_CHICK	FYN_MOUSE	RPB1_EUPOC	SOL_DROME	DSG3_HUMAN	ID	
PROBABLE SERINE/THREON		COAT PROTEIN VP1 [CONT	TRANSCRIPTION INITIATI	SCYTALONE DEHYDRATASE	50S RIBOSOMAL PROTEIN	NEUROGENIC LOCUS NOTCH	HEMAGGLUTININ-NEURAMIN	н			GLYCININ G3 PRECURSOR	~	T-COMPLEX PROTEIN 1, E				PROTO-ONCOGENE TYROSIN	PROTO-ONCOGENE TYROSIN	DNA-DIRECTED RNA POLYM	SMALL OPTIC LOBES PROT	DESMOGLEIN 3 PRECURSOR	Description	
1.22e+01	1.226+01	1.22e+01	1.22e+01			4.61e+00	٠	4.61e+00	-	2.80e+00						. 55e					3.88e-13	Pred. No.	

4.5	43	42	41	40	39	38	37	36	35	34	S S	32	ω μ	30	29	28	27	26	25	24
47	47	47	47	47	47	47	47	47	47	47	48	48	48	48	48	48	48	48	48	40
47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5
1163 2278	606	544	512	470	469	469	416	370	221	220	1591	1591	1201	1130	1125	1053	927	823	729	510
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FAB1_YEAST	TERM_ADE12	TCPH_MOUSE	AMY_BACLI	NRAM_IAWHM	NIFN_RHISN	NRAM_IAHCO	FILA_HUMAN	MAF2_MOUSE	RS8_MAIZE	RS8_ORYSA	TIAM_HUMAN	TIAM_MOUSE	COPA_YEAST	C2TA_HUMAN	PHYA_POPTM	CAPP_ANANI	CC15_SCHPO	UBPG_HUMAN	NARB_SYNP7	CATB_PSESY
PROBABLE PHOSPHATIDYLI	171		_	NEURAMINIDASE (EC 3.2.			FILAGGRIN PRECURSOR (F	TRANSCRIPTION FACTOR M	RIBOSOMAL	40S RIBOSOMAL PROTEIN	INVASION	T-LYMPHOMA INVASION AN	COATOMER ALPHA SUBUNIT	MHC CLASS II TRANSACTI	PHYTOCHROME A.	PHOSPHOENOLPYRUVATE CA	CELL DIVISION CONTROL	UBIQUITIN CARBOXYL-TER	NITRATE REDUCTASE (EC	CATALASE PRECURSOR (EC
1.97e+01 1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.97e+01	1.22e+01	1.22e+01	1.22e+01	1.22e+01	1.22e+01	1.22e+01	1.22e+01	1.22e+01	1.22e+01	1.22e+01

ALIGNMENTS

						ETDS G G G G G G G G G G G G G G G G G G G
EMBL; M76482; AAA60230.1; PIR; A41088; IJHUG3. HSSP; P09803; IEDH. MIM; 169615; PROSITE; P500232; CADHERIN; 3. PFAM; PF00028; Cadherin; 4. Cell adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein;	a collabora BL outstati ictions on is in no for commer ib.ch/annou	-1- DISEASE: PEMPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN DISEASE IN WHICH EPIDERNAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG31- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN!- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, ESOPHAGUS AND CARCINOMAS!- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS (POTENTIAL).	Amagal M., Klaus-Koytun V., Stanley J.R.; "Autoanthodies against a novel epithelial cadherin in pemphigus vulgaris, a disease of cell adhesion."; Cell 67:869-877(1991) FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION.	ppiens (Human). ota; Metazoa; Chordat la; Primates; Catarrh ce FROM N.A. c; 92069753.	1 SG3_HUMAN 32926; 1-OCT-1993 1-OCT-1993 1-NOV-1997 ESMOGLEIN 3 SG3.

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